

# SEQUENCE LISTING

<110> Kleanthous, Harold  
Al-Garawi, Amal  
Miller, Charles  
Tomb, Jean Francois  
Oomen, Raymond P.

<120> IDENTIFICATION OF POLYNUCLEOTIDES  
ENCODING NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER  
GENOME

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Val	Val	Val	Val	Thr	Ile	Ile	Pro	Met	Val	Ser	Ser	Val	Val	Val	Asn	
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Pro	Arg	His	Ser	Arg	Phe	Tyr	Val	Trp	Ser	Glu	Pro	Phe	Phe	Lys	Ala	
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Leu	Glu	Ser	Arg	Tyr	Thr	Lys	Leu	Leu	Gln	Trp	Val	Leu	Asn	His	Lys	
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Ile	Ile	Ile	Ser	Ile	Ala	Val	Val	Leu	Val	Phe	Val	Gly	Ser	Leu	Phe	
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2386

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-17-

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	Male	1.0	0	1
Marital status	Married	1.0	0	1
Education	High school	1.0	0	1
Occupation	Unemployed	1.0	0	1
Income	Low	1.0	0	1
Health status	Good	1.0	0	1
Smoking status	Non-smoker	1.0	0	1
Alcohol consumption	Non-drinker	1.0	0	1
Exercise frequency	Low	1.0	0	1
Stress level	Low	1.0	0	1
Sleep quality	Good	1.0	0	1
Dietary habits	Healthy	1.0	0	1
Family size	Small	1.0	0	1
Work-life balance	Good	1.0	0	1
Community involvement	Low	1.0	0	1
Life satisfaction	Low	1.0	0	1
Resilience	Low	1.0	0	1
Optimism	Low	1.0	0	1
Gratitude	Low	1.0	0	1
Self-compassion	Low	1.0	0	1
Emotional regulation	Low	1.0	0	1
Interpersonal relationships	Low	1.0	0	1
Personal growth	Low	1.0	0	1
Meaning in life	Low	1.0	0	1
Existential well-being	Low	1.0	0	1
Overall well-being	Low	1.0	0	1

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Ser	Tyr	Val	Val	Val	Val	Thr	Ile	Ile	Pro	Met	Val	Ser	Ser	Val	Val
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Val	Asn	Pro	Arg	His	Ser	Arg	Phe	Tyr	Val	Trp	Ser	Glu	Pro	Phe	Phe
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Lys	Ala	Leu	Glu	Ser	Arg	Tyr	Thr	Lys	Leu	Leu	Gln	Trp	Val	Leu	Asn
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Leu	Ile	Phe	Asn	Ala	Leu	Asp	Leu	Tyr	Ala	Leu	Lys	Leu	Glu	Asp
		115					120					125		Leu
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	130					135					140			Asp
Ala	Ile	Leu	Lys	Ser	Lys	Asn	Pro	Pro	Leu	Trp	Arg	Leu	Ile	Asn
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Leu	Gly	Ile	Glu	His	Ile	Gly	Lys	Gly	Ala	Ser	Lys	Thr	Leu	Ala
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Met Arg Pro Gly Val Leu Gln Val Gly Ala Met Tyr Ala Asn Gly Val	
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ggg atc caa acc aac aga tta aaa gcc gct cgc tat tat gaa tgg gtt	152
Gly Ile Gln Thr Asn Arg Leu Lys Ala Ala Arg Tyr Tyr Glu Trp Val	
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gca gcg ggg gcg atg cga ccg ctt gcg cga atc tgg ctc aga tgt atg	200
Ala Ala Gly Ala Met Arg Pro Leu Ala Arg Ile Trp Leu Arg Cys Met	
35 40 45 50	
aaa aca aga aaa atg cgg att caa acg ata aag aaa acg ctt tgc aat	248
Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu Cys Asn	
55 60 65	
tgt atg cgg tgg ctt gtc aag ggg ggg ata tgc tcg cat gca ata att	296
Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala Ile Ile	
70 75 80	
tgg ggt gga tgt ttg cta acg gaa gtg ggg tcc caa aag att att aca	344
Trp Gly Gly Cys Leu Leu Thr Glu Val Gly Ser Gln Lys Ile Ile Thr	
85 90 95	
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Lys Arg	
100	
aat	403



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 <212> PRT  
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 35 40 45  
 Cys Met Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu  
 50 55 60  
 Cys Asn Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala  
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 Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg  
 5 10 15  
 att gaa gtg atc gta gat gat gat aac gtg atc act gat gcg ttt tct 152  
 Ile Glu Val Ile Val Asp Asp Asp Asn Val Ile Thr Asp Ala Phe Ser  
 20 25 30  
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 Ser Ser Thr Leu Phe Arg Gly Leu Glu Thr Ile Ile Lys Gly Arg Asp  
 35 40 45 50  
 cca cga gat gca ggc ttc atc gct caa agg att tgc ggg gta tgc act 248  
 Pro Arg Asp Ala Gly Phe Ile Ala Gln Arg Ile Cys Gly Val Cys Thr  
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 Tyr Ser His Tyr Lys Ala Gly Ile Thr Ala Val Glu Asn Ala Leu Gly  
 70 75 80  
 atc act ccc cca tta aac gcg caa ttg gtg cga tct ttg atg aac atg 344  
 Ile Thr Pro Pro Leu Asn Ala Gln Leu Val Arg Ser Leu Met Asn Met  
 85 90 95

gcg ctg ctt ttt cat gac cat gtg gtg cat ttc tat act ttg cat ggg Ala Leu Leu Phe His Asp His Val Val His Phe Tyr Thr Leu His Gly 100 105 110	392
ctt gat tgg tgc gat atc atg agc gct tta aaa gcc gat ccc att caa Leu Asp Trp Cys Asp Ile Met Ser Ala Leu Lys Ala Asp Pro Ile Gln 115 120 125 130	440
gcg gca aaa ctt tct ttc aaa tac agc cct tac cct att aat acc ggt Ala Ala Lys Leu Ser Phe Lys Tyr Ser Pro Tyr Pro Ile Asn Thr Gly 135 140 145	488
gcc ggt gaa tta aaa gcg gtt caa aaa cgc ttg agc gat ttc gct aaa Ala Gly Glu Leu Lys Ala Val Gln Lys Arg Leu Ser Asp Phe Ala Lys 150 155 160	536
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tat cgt tta agt ccg gag caa aat tta atc gtc tta agc cac tac ctc Tyr Arg Leu Ser Pro Glu Gln Asn Leu Ile Val Leu Ser His Tyr Leu 180 185 190	632
aag ctt tta gaa atc caa agg gaa gcg gcg aaa atg acc gct att ttt Lys Leu Leu Glu Ile Gln Arg Glu Ala Ala Lys Met Thr Ala Ile Phe 195 200 205 210	680
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agt gtt atg gat ata ttg gat ccg acg aga ttg gct gaa tgg aag agc Ser Val Met Asp Ile Leu Asp Pro Thr Arg Leu Ala Glu Trp Lys Ser 230 235 240	776
aag ttt gaa gtg gtg gcc aat ttc atc aac cat gct tac tac cct gat Lys Phe Glu Val Val Ala Asn Phe Ile Asn His Ala Tyr Tyr Pro Asp 245 250 255	824
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ggc tgt ggc tta agg aat ttt atc gct tat gaa gaa gtg ctg ctt ggg Gly Cys Gly Leu Arg Asn Phe Ile Ala Tyr Glu Glu Val Leu Leu Gly 275 280 285 290	920
agg gat aaa tac ctt ttg agt agt ggg gtg gtg ctt gat ggg gat att Arg Asp Lys Tyr Leu Leu Ser Ser Gly Val Val Leu Asp Gly Asp Ile 295 300 305	968
tct aaa tta cac ccc att gat gaa agt ttg att aaa gaa gaa gtt acg Ser Lys Leu His Pro Ile Asp Glu Ser Leu Ile Lys Glu Glu Val Thr 310 315 320	1016
cat tct tgg tat caa tac gaa gac act aaa gaa gtg caa ctc cac cct His Ser Trp Tyr Gln Tyr Glu Asp Thr Lys Glu Val Gln Leu His Pro 325 330 335	1064

tat gac ggg caa acg aac ccg cat tat acc ggt tta aaa gac ggc gag Tyr Asp Gly Gln Thr Asn Pro His Tyr Thr Gly Leu Lys Asp Gly Glu 340 345 350	1112
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atg gaa gta ggt cct tta agt tcc gta gtg gta ggt tta gcg gcg aaa Met Glu Val Gly Pro Leu Ser Ser Val Val Val Gly Leu Ala Ala Lys 390 395 400	1256
aac cct tat gtt act gaa gtg gct acg aag ttt tta aaa gac act aaa Asn Pro Tyr Val Thr Glu Val Ala Thr Lys Phe Leu Lys Asp Thr Lys 405 410 415	1304
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gcg tta gtg gaa aat cta aaa agc gat caa agc act tgt gct cct tat Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala Pro Tyr 455 460 465	1448
cac att gat aaa aat caa gaa tat aaa ggg cgc tac att ggt caa gtg His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly Gln Val 470 475 480	1496
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gaa aat tat caa gcg gtg gtg cct tct act tgg aat gca ggg cct aga Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly Pro Arg 500 505 510	1592
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aaa atc gct gat tta acc cag cct tta gaa atc att agg act atc cat Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr Ile His 535 540 545	1688
tct ttt gac cca tgc atc gca tgc tcg gtg cat gtg atg gat ttt aaa Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp Phe Lys 550 555 560	1736
ggg cag tct tta aac gag ttt aaa gta gag cct aat ttc gct aaa ttc Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala Lys Phe	1784

565

570

575

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1837

&lt;210&gt; 18

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 18

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			20					25					30		
Phe	Ser	Ser	Ser	Thr	Leu	Phe	Arg	Gly	Leu	Glu	Thr	Ile	Ile	Lys	Gly
		35					40					45			
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	50					55				60					
Cys	Thr	Tyr	Ser	His	Tyr	Lys	Ala	Gly	Ile	Thr	Ala	Val	Glu	Asn	Ala
65					70					75				80	
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				85				90					95		
Asn	Met	Ala	Leu	Leu	Phe	His	Asp	His	Val	Val	His	Phe	Tyr	Thr	Leu
			100					105					110		
His	Gly	Leu	Asp	Trp	Cys	Asp	Ile	Met	Ser	Ala	Leu	Lys	Ala	Asp	Pro
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Thr	Gly	Ala	Gly	Glu	Leu	Lys	Ala	Val	Gln	Lys	Arg	Leu	Ser	Asp	Phe
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Ala	Lys	Ser	Gly	Ser	Leu	Gly	Pro	Phe	Ser	Asn	Gly	Tyr	Tyr	Gly	His
				165				170						175	
Lys	Thr	Tyr	Arg	Leu	Ser	Pro	Glu	Gln	Asn	Leu	Ile	Val	Leu	Ser	His
			180					185					190		
Tyr	Leu	Lys	Leu	Leu	Glu	Ile	Gln	Arg	Glu	Ala	Ala	Lys	Met	Thr	Ala
		195					200					205			
Ile	Phe	Gly	Ala	Lys	Gln	Pro	His	Pro	Gln	Ser	Leu	Thr	Val	Gly	Gly
	210					215					220				
Val	Thr	Ser	Val	Met	Asp	Ile	Leu	Asp	Pro	Thr	Arg	Leu	Ala	Glu	Trp
225					230					235				240	
Lys	Ser	Lys	Phe	Glu	Val	Val	Ala	Asn	Phe	Ile	Asn	His	Ala	Tyr	Tyr
				245					250					255	
Pro	Asp	Leu	Val	Met	Ala	Gly	Glu	Met	Phe	Ala	Asn	Glu	Gln	Ser	Val
			260					265					270		
Ile	Lys	Gly	Cys	Gly	Leu	Arg	Asn	Phe	Ile	Ala	Tyr	Glu	Glu	Val	Leu
		275					280					285			
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	290					295					300				
Asp	Ile	Ser	Lys	Leu	His	Pro	Ile	Asp	Glu	Ser	Leu	Ile	Lys	Glu	Glu
305					310					315				320	
Val	Thr	His	Ser	Trp	Tyr	Gln	Tyr	Glu	Asp	Thr	Lys	Glu	Val	Gln	Leu
				325					330					335	
His	Pro	Tyr	Asp	Gly	Gln	Thr	Asn	Pro	His	Tyr	Thr	Gly	Leu	Lys	Asp
			340					345					350		
Gly	Glu	Ser	Val	Gly	Ile	Glu	Asn	Lys	Ile	Ile	Pro	Ala	Lys	Val	Leu
		355					360					365			
Asp	Thr	Lys	Asn	Lys	Tyr	Ser	Trp	Ile	Lys	Ser	Pro	Arg	Tyr	Asp	Ser
	370					375					380				
Lys	Pro	Met	Glu	Val	Gly	Pro	Leu	Ser	Ser	Val	Val	Val	Gly	Leu	Ala

385					390					395				400
Ala	Lys	Asn	Pro	Tyr	Val	Thr	Glu	Val	Ala	Thr	Lys	Phe	Leu	Lys
				405					410					415
Thr	Lys	Leu	Pro	Leu	Glu	Ala	Leu	Phe	Ser	Thr	Leu	Gly	Arg	Thr
			420					425					430	
Ala	Arg	Cys	Ile	Glu	Ala	Lys	Thr	Ile	Ala	Asp	Asn	Gly	Leu	Leu
		435					440					445		
Phe	Asp	Ala	Leu	Val	Glu	Asn	Leu	Lys	Ser	Asp	Gln	Ser	Thr	Cys
	450					455				460				
Pro	Tyr	His	Ile	Asp	Lys	Asn	Gln	Glu	Tyr	Lys	Gly	Arg	Tyr	Ile
465					470					475				480
Gln	Val	Pro	Arg	Gly	Met	Leu	Ser	His	Trp	Val	Arg	Ile	Lys	Asn
				485					490					495
Val	Val	Glu	Asn	Tyr	Gln	Ala	Val	Val	Pro	Ser	Thr	Trp	Asn	Ala
		500						505					510	
Pro	Arg	Asp	Ser	Gln	Asn	Gln	Arg	Gly	Ala	Tyr	Glu	Met	Ser	Leu
		515					520					525		
Gly	Thr	Lys	Ile	Ala	Asp	Leu	Thr	Gln	Pro	Leu	Glu	Ile	Ile	Arg
	530					535					540			
Ile	His	Ser	Phe	Asp	Pro	Cys	Ile	Ala	Cys	Ser	Val	His	Val	Met
545					550					555				560
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Lys	Phe													

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 <222> (80)...(613)

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Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly	
1 5 10	
aat atc ctt ttt ggc gat gaa ggg att ggg gtg cat tta gcc cac tac	160
Asn Ile Leu Phe Gly Asp Glu Gly Ile Gly Val His Leu Ala His Tyr	
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Leu Lys Lys Asn Phe Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly	
30 35 40	
ggg aca atg gcc cag cag ctc att cct tta atc act tcg tat gaa aag	256
Gly Thr Met Ala Gln Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys	
45 50 55	
ggt ttg att ttg gat tgc gtg agc gct gaa ggc gtt gag ata gga tca	304
Val Leu Ile Leu Asp Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser	
60 65 70 75	
gtc tat gct ttt gat ttt aag gac gct cct aaa gaa atc aca tgg gct	352
Val Tyr Ala Phe Asp Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala	

	80						85							90										
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ttt tta ggg gat ttg cct aaa act ttt atc gtg ggg ctt gtg cct ttt Phe Leu Gly Asp Leu Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe	110						115							120									448	
gtg ata ggg agc gag acc act ttc aag ctt tca agc aaa att tta aac Val Ile Gly Ser Glu Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn	125						130							135									496	
gct tta gaa acc gcc tta aaa gcc ata gaa acc caa ctg aac gca tgg Ala Leu Glu Thr Ala Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp	140						145							150									155	544
ggg gtt aaa atg caa cgc acc gat cat atc gct tta gaa tgt atc gct Gly Val Lys Met Gln Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala	160						165							170									592	
gaa ctt tct tat aag ggt ttt tgaattgggtt tttgttttttc tttttaaatg Glu Leu Ser Tyr Lys Gly Phe	175																643							
cgттаатгаа гааасагсс тгааттттаc гссстттта gaгсаатгг саtgчааттt гсаагсгсгт ттттата																					703 720			
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Ser Phe Phe Pro Ser Val Asp Ile Asp Gly Gly Thr Met Ala Gln 35                40                45																								
Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp 50                55                60																								
Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp 65                70                75                80																								
Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu 85                90                95																								
Val Glu Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu 100                105                110																								
Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu 115                120                125																								
Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala 130                135                140																								
Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln 145                150                155                160																								
Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys 165                170                175																								
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[illegible]

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-34-



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aac Asn	aaa Lys	cct Pro	ttt Phe 150	gaa Glu	ttg Leu	gtg Val	cta Leu	gaa Glu 155	gac Asp	atg Met	ctc Leu	aaa Lys	gcc Ala 160	ggg Gly	gtg Val	536
gat Asp	tcc Ser	atg Met 165	cct Pro	ggt Gly	ggg Gly	ggg Gly	gcg Ala 170	gag Glu	att Ile	ttt Phe	gat Asp 175	gaa Glu	gaa Glu	atc Ile	agg Arg	584
cgt Arg	aaa Lys 180	atc Ile	tgt Cys	aat Asn	ggt Gly	aag Lys 185	gtg Val	gga Gly	tct Ser	tct Ser	cgg Arg 190	tgg Trp	tta Leu	gaa Glu	atc Ile	632
cat His 195	gct Ala	tat Tyr	tgg Trp	cac His	aaa Lys 200	tta Leu	ggc Gly	aaa Lys	atg Met 205	agt Ser	aac Asn	gct Ala	acc Thr	atg Met	ctt Leu 210	680
ttt Phe	ggg Gly	cat His	att Ile	gaa Glu 215	aat Asn	aaa Lys	atc Ile	cat His	cgc Arg 220	atc Ile	gat Asp	cac His	atg Met	cta Leu 225	aga Arg	728
atc Ile	aaa Lys	aaa Lys	atc Ile 230	caa Gln	agc Ser	cct Pro	aaa Lys	aat Asn 235	caa Gln	gta Val	gaa Glu	aac Asn	aaa Lys 240	gaa Glu	ggg Gly	776
ggt Gly	ttt Phe	aac Asn 245	gct Ala	ttt Phe	atc Ile	ccc Pro	ttg Leu 250	ttg Leu	tat Tyr	caa Gln	aaa Lys	gaa Glu 255	aac Asn	aat Asn	tat Tyr	824
ttg Leu	aat Asn 260	gtg Val	gaa Glu	aaa Lys	tcc Ser	ccc Pro	agt Ser 265	gcg Ala	ata Ile	gaa Glu	atc Ile 270	tta Leu	aaa Lys	acc Thr	atc Ile	872
gcc Ala 275	ata Ile	tct Ser	cgc Arg	att Ile	ctt Leu 280	tta Leu	aac Asn	aat Asn	atc Ile	cct Pro 285	cac His	att Ile	aaa Lys	gct Ala	tat Tyr 290	920
tgg Trp	gcg Ala	act Thr	ttg Leu	ggc Gly 295	ttg Leu	aat Asn	ttg Leu	gct Ala	tta Leu 300	gtg Val	gct Ala	caa Gln	gaa Glu	ttt Phe 305	ggc Gly	968
gct Ala	aac Asn	gat Asp 310	tta Leu	gac Asp	ggc Gly	acg Thr	ata Ile	gag Glu 315	ata Ile	gag Glu	agc Ser	att Ile	caa Gln 320	agc Ser	gcg Ala	1016
gca Ala	ggc Gly	gca Ala 325	aag Lys	agc Ser	cgg Arg	cat His	ggt Gly 330	tta Leu	gaa Glu	aaa Lys	gaa Glu	gat Asp 335	ttg Leu	ata Ile	ttt Phe	1064
aaa Lys	atc Ile	aag Lys	gac Asp	gct Ala	ggt Gly	ttt Phe	gtt Val	gcg Ala	gta Val	gaa Glu	agg Arg	gat Asp	agt Ser	ttg Leu	tat Tyr	1112



355

360

&lt;210&gt; 25

&lt;211&gt; 616

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51)...(563)

&lt;400&gt; 25

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Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys Leu Ile	
5 10 15	
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His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys Ile Ser	
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Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys Lys Asn	
35 40 45 50	
gaa gct tat ttt att tct gat gaa gaa gat aaa aat tat gtt ttg gtg	248
Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val Leu Val	
55 60 65	
cca gat aac gtg atc tct ctt ttg gca gaa aac gcc aga aag gct ttt	296
Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys Ala Phe	
70 75 80	
gaa gcc agg ctt agg gcg gaa tta gaa agg gat att atc acc caa gcg	344
Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr Gln Ala	
85 90 95	
ccg att gat ttt gaa gac gtg cgc gaa gtt tcc ttg caa cta ttg gaa	392
Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu Leu Glu	
100 105 110	
aat tta cgc caa aaa gat ggg aat ttg cct aat atc aac acc tta aac	440
Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr Leu Asn	
115 120 125 130	
ttt gtc aaa caa atc aaa aaa gaa cac cct aat tta ttc ttt aat ttt	488
Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe Asn Phe	
135 140 145	
gac aac atg ttc aaa caa ccc cct ttt aat gag aat aat ttt gaa aat	536
Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe Glu Asn	
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Phe Asp Asn Ser Asp Glu Glu Asn Phe	
165 170	

616

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Glu	Asn	Ile	Asn	Glu	Asn	Ile	Phe	Glu	Glu	Val	Gly	Asp	Ala	Cys	Val		
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aaa tgc gct aag tgc gtg cca ggc tgc acc ata tac cgc att cat aaa																	152
Lys	Cys	Ala	Lys	Cys	Val	Pro	Gly	Cys	Thr	Ile	Tyr	Arg	Ile	His	Lys		
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gac gag gcg act tcg cct aga ggc ttt tta gat ttg atg cgc tta aac																	200
Asp	Glu	Ala	Thr	Ser	Pro	Arg	Gly	Phe	Leu	Asp	Leu	Met	Arg	Leu	Asn		
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gct caa aac aag ctc caa tta gac acg aat tta aaa cac ctt tta gaa																	248

Ala	Gln	Asn	Lys	Leu	Gln	Leu	Asp	Thr	Asn	Leu	Lys	His	Leu	Leu	Glu		
				55					60					65			
act	tgc	ttt	tta	tgc	acc	gct	tgc	gtg	gaa	att	tgc	cct	ttt	cat	ttg		296
Thr	Cys	Phe	Leu	Cys	Thr	Ala	Cys	Val	Glu	Ile	Cys	Pro	Phe	His	Leu		
			70					75					80				
ccc	ata	gac	acc	tta	ata	gaa	aaa	gcc	aga	gaa	aaa	atc	gct	caa	aag		344
Pro	Ile	Asp	Thr	Leu	Ile	Glu	Lys	Ala	Arg	Glu	Lys	Ile	Ala	Gln	Lys		
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cat	ggc	atc	gct	tggt	tat	aaa	aaa	tcc	tat	ttt	tcc	ctt	tta	aaa	aac		392
His	Gly	Ile	Ala	Trp	Tyr	Lys	Lys	Ser	Tyr	Phe	Ser	Leu	Leu	Lys	Asn		
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cgc	aaa	aaa	atg	gat	agg	gtg	ttt	tca	act	gcg	cat	ttt	tta	gcc	cct		440
Arg	Lys	Lys	Met	Asp	Arg	Val	Phe	Ser	Thr	Ala	His	Phe	Leu	Ala	Pro		
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Cys	Val	Phe	Lys	Gln	Val	Gly	Asp	Ser	Leu	Glu	Pro	Arg	Ala	Val	Phe		
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aaa	ggt	ttg	ttc	aaa	cgc	ttt	aaa	aaa	agc	gcg	ctg	cct	cct	tta	aat		536
Lys	Gly	Leu	Phe	Lys	Arg	Phe	Lys	Lys	Ser	Ala	Leu	Pro	Pro	Leu	Asn		
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Gln	Lys	Ser	Phe	Leu	Gln	Lys	His	Ala	Glu	Met	Lys	Leu	Leu	Glu	Asn		
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ccc	att	caa	aaa	gtg	gcc	att	ttt	ata	ggg	tgc	ttg	agc	aat	tac	cat		632
Pro	Ile	Gln	Lys	Val	Ala	Ile	Phe	Ile	Gly	Cys	Leu	Ser	Asn	Tyr	His		
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Tyr	Gln	Gln	Val	Gly	Glu	Ser	Leu	Leu	Tyr	Ile	Leu	Glu	Lys	Leu	Asn		
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Ile	Gln	Ala	Ile	Ile	Pro	Lys	Gln	Glu	Cys	Cys	Ser	Ala	Pro	Ala	Tyr		
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Phe	Thr	Gly	Asp	Lys	Asp	Thr	Thr	Leu	Phe	Leu	Val	Lys	Lys	Asn	Ile		
			230					235					240				
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Glu	Trp	Phe	Glu	Ser	Tyr	Leu	Asp	Lys	Val	Asp	Ala	Ile	Ile	Val	Pro		
		245					250					255					
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Glu	Ala	Thr	Cys	Ala	Thr	Cys	Ser	Ser	Thr	Ile	Ile	Thr	Arg	Cys	Phe		
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Trp	Ala	Lys	Lys	Ile	Arg	Ile	Cys	Met									
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His Lys Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg  
35 40 45  
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50 55 60  
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65 70 75 80  
His Leu Pro Ile Asp Thr Leu Ile Glu Lys Ala Arg Glu Lys Ile Ala  
85 90 95  
Gln Lys His Gly Ile Ala Trp Tyr Lys Lys Ser Tyr Phe Ser Leu Leu  
100 105 110  
Lys Asn Arg Lys Lys Met Asp Arg Val Phe Ser Thr Ala His Phe Leu  
115 120 125  
Ala Pro Cys Val Phe Lys Gln Val Gly Asp Ser Leu Glu Pro Arg Ala  
130 135 140  
Val Phe Lys Gly Leu Phe Lys Arg Phe Lys Lys Ser Ala Leu Pro Pro  
145 150 155 160  
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165 170 175  
Glu Asn Pro Ile Gln Lys Val Ala Ile Phe Ile Gly Cys Leu Ser Asn  
180 185 190  
Tyr His Tyr Gln Gln Val Gly Glu Ser Leu Leu Tyr Ile Leu Glu Lys  
195 200 205  
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210 215 220  
Ala Tyr Phe Thr Gly Asp Lys Asp Thr Thr Leu Phe Leu Val Lys Lys  
225 230 235 240  
Asn Ile Glu Trp Phe Glu Ser Tyr Leu Asp Lys Val Asp Ala Ile Ile  
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Val Pro Glu Ala Thr Cys Ala Thr Cys Ser Ser Thr Ile Ile Thr Arg  
260 265 270  
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Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp Ile Arg Lys	
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Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro Asp Val Leu	
20 25 30 35	
tct ctt gtt gct gat tgt att tta gag ttt acg caa tgt aat att gga	201
Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys Asn Ile Gly	
40 45 50	
aaa tca ttt tct att agg gat att tgg gat agc cct tac acc aat gaa	249
Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr Thr Asn Glu	
55 60 65	
aat gtt aaa atg att ttt tct aaa cct gat tta aat tct gac ttt tcc	297
Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser Asp Phe Ser	
70 75 80	
atg cat gaa tac gat aag ttt ttt tct cag cct att aaa tta tta gcc	345
Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys Leu Leu Ala	
85 90 95	
tat agc ggt att tta ttt gaa aca aaa act ggc aat aga aat att tat	393
Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg Asn Ile Tyr	
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Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln Arg Glu Thr	
120 125 130	
aac gct ttg aaa ttc ctt att tta tat att caa aag gta tta atg gat	489
Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val Leu Met Asp	
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Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys Gln Asp Thr	
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Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe Thr Ile Asn	
165 170 175	
aac aca gca atc aat aac gct acg gaa tgt ttt agg att ttt act aaa	633
Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile Phe Thr Lys	
180 185 190 195	
att atc aat cct tta gct ttt tat tat ggt aaa aaa ggc aca aga aaa	681
Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly Thr Arg Lys	
200 205 210	
ggg tat ttg tcc aac act ata att aca aaa gat gag ctt aat tat aat	729
Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu Asn Tyr Asn	
215 220 225	
cgt atc aat tgg cga gat ata gga aaa gat aaa aat acc acc aga caa	777
Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr Thr Arg Gln	
230 235 240	

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att tca aaa gct aag aaa gtg gtg aaa cga tat aat gat aga ttt aat Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn 260 265 270 275																873
aat tct ctc tct gaa gta aaa caa gaa aaa gaa gag tcg caa gcc aca Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr 280 285 290																921
caa ata cac cat att ttt ccc atc caa gac ttt ccc att att gct aac Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile Ile Ala Asn 295 300 305																969
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gcc cac cct aat aat caa acc cgc ttg att gat aaa gat ttt caa tat Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr 325 330 335																1065
atc tgc tta tta gct aaa acg acc aca att ctt aat gac act caa ggc Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly 340 345 350 355																1113
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tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe 405 410 415																1305
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Ile	Arg	Lys	Thr	Gln	Asn	Ala	Arg	Trp	Ile	Asp	Gln	Lys	Cys	Thr	Pro
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Asp	Val	Leu	Ser	Leu	Val	Ala	Asp	Cys	Ile	Leu	Glu	Phe	Thr	Gln	Cys
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Asn	Ile	Gly	Lys	Ser	Phe	Ser	Ile	Arg	Asp	Ile	Trp	Asp	Ser	Pro	Tyr
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65					70					75					80
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Leu	Leu	Ala	Tyr	Ser	Gly	Ile	Leu	Phe	Glu	Thr	Lys	Thr	Gly	Asn	Arg
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Gln	Asp	Thr	Glu	Ser	Phe	Lys	Gln	Leu	Lys	Asp	Gly	Phe	Thr	His	Phe
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			180					185					190		
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Asn	Tyr	Leu	Ile	Ser	Lys	Ala	Lys	Lys	Val	Val	Lys	Arg	Tyr	Asn	Asp
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	275						280					285			
Gln	Ala	Thr	Gln	Ile	His	His	Ile	Phe	Pro	Ile	Gln	Asp	Phe	Pro	Ile
	290					295					300				
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Phe	Ile	Tyr	Ala	His	Pro	Asn	Asn	Gln	Thr	Arg	Leu	Ile	Asp	Lys	Asp
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Phe	Gln	Tyr	Ile	Cys	Leu	Leu	Ala	Lys	Thr	Thr	Thr	Ile	Leu	Asn	Asp
			340					345					350		
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	370					375					380				
Leu	Lys	Val	Ile	Asp	Ala	Phe	Tyr	Phe	Asp	Phe	Asn	Lys	Ser	Lys	Asp
385					390					395					400
Pro	Ser	Trp	Ser	Tyr	Leu	Leu	Asp	Lys	Asn	Asp	Leu	Arg	Ala	Phe	Lys
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gcg att aga gat aca ggg cat ttt ttg gat tgc tct ttt gat att cat	154
Ala Ile Arg Asp Thr Gly His Phe Leu Asp Cys Ser Phe Asp Ile His 20 25 30	
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Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu Phe Phe 35 40 45 50	
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Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys Asp Met 55 60 65	
ggg aaa gaa atc aac tat ttg agt gtt tgc acg cct acg cac acg cat	298
Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His Thr His 70 75 80	
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Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val Ile Cys 85 90 95	
gaa aaa ccc tta gtt tta gac cct ggc gaa ata caa gaa ttg aaa gat	394
Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu Lys Asp 100 105 110	
tta gag gtg aaa cac caa aaa agg gtg ttt agt ctt tta ccc ttg cgc	442
Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro Leu Arg 115 120 125 130	
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gac aaa aac cct agc aag gtg ttt gac atc acg ctc act tat atc agc	538
Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr Ile Ser 150 155 160	
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Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val Asn Arg 165 170 175	
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Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp Thr Leu 180 185 190	
atc tat ttg ttt gga agc gtt aaa gac aag gtt atc aat aaa gaa gag	682
Ile Tyr Leu Phe Gly Ser Val Lys Asp Lys Val Ile Asn Lys Glu Glu 195 200 205 210	
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763

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35 40 45  
Phe Phe Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys  
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Asp Met Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His  
65 70 75 80  
Thr His Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val  
85 90 95  
Ile Cys Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu  
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Lys Asp Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro  
115 120 125  
Leu Arg Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser  
130 135 140  
Glu Leu Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr  
145 150 155 160  
Ile Ser Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val  
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gcc Ala	ctt Leu	att Ile	ttg Leu 70	gtg Val	ttg Leu	ggg Gly	cag Gln	gct Ala 75	ctg Leu	gct Ala	aac Asn	gct Ala	aaa Lys 80	tta Leu	gtc Val	296
caa Gln	aag Lys	ctt Leu 85	tta Leu	aaa Lys	tat Tyr	cta Leu	gcg Ala 90	tct Ser	tta Leu	cct Pro	aaa Lys	ggg Gly 95	tat Tyr	tat Tyr	acg Thr	344
gct Ala 100	tta Leu	tgg Trp	ttg Leu	gtt Val	act Thr	ttt Phe 105	tta Leu	tcg Ser	tta Leu	atc Ile	gct Ala 110	aat Asn	tgg Trp	atc Ile	aac Asn	392
tgg Trp 115	ggg Gly	ttt Phe	ggc Gly	ttg Leu	gtg Val 120	att Ile	agt Ser	gcg Ala	att Ile	ttt Phe 125	gca Ala	aaa Lys	gag Glu	atc Ile	gcc Ala 130	440
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tcg Ser	ggg Gly	ttt Phe 150	gtc Val	atc Ile	tgg Trp	cat His	ggg Gly 155	ggg Gly	tta Leu	tca Ser	ggc Gly	tct Ser	atc Ile 160	cct Pro	tta Leu	536
agc Ser	gtt Val	gcc Ala 165	acc Thr	caa Gln	aat Asn	gaa Glu	aat Asn 170	cta Leu	tcc Ser	aaa Lys	ata Ile	agc Ser 175	gct Ala	ggg Gly	gtg Val	584
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tta Leu 195	atc Ile	att Ile	ata Ile	ggg Gly 200	atc Ile	att Ile	ctt Leu	gta Val	ggg Gly 205	tta Leu 210	ccc Pro	ttt Phe	tta Leu	atg Met	gca Ala 210	680
atg Met	atc Ile	cac His	cct Pro	aaa Lys 215	aaa Lys	gaa Glu	gaa Glu	atc Ile	ggt Val 220	gag Glu	att Ile	gat Asp	tca Ser	aag Lys 225	ctt Leu	728
tta Leu	aaa Lys	gac Asp	gag Glu 230	tac Tyr	aaa Lys	gag Glu	att Ile	gaa Glu 235	ctc Leu	att Ile	agc Ser	cac His	caa Gln 240	caa Gln	gac Asp	776
aaa Lys	acg Thr	atc Ile 245	gcg Ala	cat His	ttt Phe	ttg Leu	gaa Glu 250	aac Asn	agc Ser	gct Ala	ttg Leu 255	ctt Leu	tct Ser	tat Tyr	ctt Leu	824
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Val	Phe	Val	Leu	Val	Tyr	Cys	Leu	Thr	Gly	Gln	Asp	Ala	Phe	Ser	Val						
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Tyr	Thr	Ala	Leu	Trp	Leu	Val	Thr	Phe	Leu	Ser	Leu	Ile	Ala	Asn	Trp						
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Gly	Val	Ile	Glu	Lys	Ala	Ile	Pro	Ile	Ser	Gln	Thr	Ile	Phe	Ser	Ser						
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Tyr	Asn	Leu	Ile	Ile	Ile	Gly	Ile	Ile	Leu	Val	Gly	Leu	Pro	Phe	Leu						
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Met	Ala	Met	Ile	His	Pro	Lys	Lys	Glu	Glu	Ile	Val	Glu	Ile	Asp	Ser						
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225				230						235					240						
Gln	Asp	Lys	Thr	Ile	Ala	His	Phe	Leu	Glu	Asn	Ser	Ala	Leu	Leu	Ser						
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Tyr	Leu	Leu	Val	Phe	Leu	Gly	Phe	Gly	Tyr	Leu	Gly	Val	Tyr	Phe	Phe						
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Lys	Gly	Gly	Gly	Ile	Ser	Leu	Asn	Ile	Val	Asn	Thr	Ile	Phe	Leu	Phe						
		275					280					285									
Leu	Gly	Ile	Leu	Leu	His	Lys	Thr	Pro	Leu	Ala	Tyr	Val	Lys	Ala	Ile						
	290					295					300										
Asp	Arg	Ser	Ala	Xaa	Ser	Val	Ala	Gly	Ile	Leu	Gln	Phe	Pro	Phe							
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Tyr	Ala	Gly	Ile	Met	Gly	Met	Met	Ala	Ser	His	Ser	Val	Gly	Gly	His						
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Ser	Leu	Ala	Gln	Met	Leu	Ser	Leu	Ala	Phe	Thr	His	Ile	Ala	Asn	Glu						
			340					345					350								
Lys	Thr	Phe	Val	Leu	Met	Thr	Phe	Leu	Ser	Ala	Gly	Ile	Val	Asn	Ile						
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180			185			190												
aaa Lys 195	gac Asp	gct Ala	aaa Lys	gcc Ala	ata Ile 200	gaa Glu	gag Glu	ttg Leu	caa Gln	gac Asp 205	aaa Lys	ctg Leu	cgt Arg	ttt Phe	tca Ser 210	680		
gcg Ala	cca Pro	aag Lys	ttg Leu	ggc Gly 215	gtt Val	tct Ser	atc Ile	caa Gln	gcg Ala 220	cac His	cat His	ctt Leu	aaa Lys	aac Asn 225	ctt Leu	728		
ttg Leu	gaa Glu	gcc Ala	ttt Phe 230	tat Tyr	cac His	caa Gln	aat Asn	aaa Lys 235	gag Glu	agt Ser	ttg Leu	ggc Gly	ttt Phe 240	ttt Phe	tcc Ser	776		
cct Pro	tat Tyr	ttt Phe 245	agt Ser	ttg Leu	cga Arg	tct Ser	caa Gln 250	acc Thr	cct Pro	agc Ser	gtc Val	tct Ser 255	tat Tyr	gaa Glu	agc Ser	824		
gcg Ala 260	tta Leu	gct Ala	tct Ser	tta Leu	gaa Glu 265	aac Asn	tat Tyr	ttt Phe	atg Met	gct Ala 270	ttg Leu	ttc Phe	caa Gln	tcc Ser	cat His	872		
ttt Phe 275	aaa Lys	gac Asp	gat Asp	acc Thr	gca Ala 280	ctc Leu	caa Gln	cag Gln	aat Asn	ttt Phe 285	aaa Lys	gga Gly	ttg Leu	ttg Leu	caa Gln 290	920		
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<212> PRT
<213> Helicobacter pylori
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Tyr	Leu	Asn	Ala	Tyr	Leu	Asp	Gln	Arg	Pro	His	Ile	Lys	Gly	Met	Gly	
Ile	Ala	Gly	Thr	Pro	Phe	Glu	Cys	Glu	Gly	Phe	Phe	Lys	Ile	Ala	Cys	
Val 65	Ser	Lys	Glu	Leu	Ser	Phe	Leu	Asp	Ser	Gln	Asn	Ser	Pro	Ile	Val	
Asn	Phe	Lys	Asn	Leu	Ser	Ile	Lys	Leu	Arg	Ser	Leu	Asp	Lys	Ser	Ser	
Leu	Thr	Leu	Ser	Val	His	Ser	Gln	Ile	Lys	Ser	Pro	Ile	Leu	Glu	Gln	





Ala Phe Leu Ala Leu Leu Ala Pro Lys Ile Tyr Leu Ser Asn Asn Ile	
55 60 65	
tat tat att agc cgt aaa atc aac acc cta gaa gat caa aaa cgc ctg	296
Tyr Tyr Ile Ser Arg Lys Ile Asn Thr Leu Glu Asp Gln Lys Arg Leu	
70 75 80	
ctt tta gaa gag caa caa atc cta aaa aac gaa tta gaa aaa gag cgt	344
Leu Leu Glu Glu Gln Gln Ile Leu Lys Asn Glu Leu Glu Lys Glu Arg	
85 90 95	
ttt aaa tac tac ata gaa aat agt gaa aat att ggc gat att gcg ttt	392
Phe Lys Tyr Tyr Ile Glu Asn Ser Glu Asn Ile Gly Asp Ile Ala Phe	
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 <213> Helicobacter pylori

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Asn Ser His Gly Leu Ser Leu Met Ala Leu Ile Gly Val Leu Val Phe	
35 40 45	
Gly Gly Ala Phe Leu Ala Leu Leu Ala Pro Lys Ile Tyr Leu Ser Asn	
50 55 60	
Asn Ile Tyr Tyr Ile Ser Arg Lys Ile Asn Thr Leu Glu Asp Gln Lys	
65 70 75 80	
Arg Leu Leu Leu Glu Glu Gln Gln Ile Leu Lys Asn Glu Leu Glu Lys	
85 90 95	
Glu Arg Phe Lys Tyr Tyr Ile Glu Asn Ser Glu Asn Ile Gly Asp Ile	
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Ala Phe	

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Ile Ala His Lys Ala Gln Ser Ala Asn Gln Lys His Ile Ile Pro Ser	
5 10 15	
cat ccc cct ttc cac aat aaa caa gga ttg cgc ccc cac cgc cgc aca	153

His Pro Pro Phe His Asn Lys Gln Gly Leu Arg Pro His Arg Arg Thr  
 20 25 30  
 caa aga aat cgc taaacaaaa ccttctataa aaaccacaaa catcttgctt 205  
 Gln Arg Asn Arg  
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 aatcctttca ctc 218  
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 <211> 38  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 40  
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 1 5 10 15  
 Pro Ser His Pro Pro Phe His Asn Lys Gln Gly Leu Arg Pro His Arg  
 20 25 30  
 Arg Thr Gln Arg Asn Arg  
 35  
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 <211> 967  
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 Gly Ile Leu Glu Pro Leu Gly Ala Asn Tyr Leu Thr Leu Leu Met Val  
 5 10 15  
 tgg atc cct acg act ttt tta gca tgc atg ctc acg gca ttt att atg 152  
 Trp Ile Pro Thr Thr Phe Leu Ala Cys Met Leu Thr Ala Phe Ile Met  
 20 25 30  
 ggt ttt act gat ttg aaa tta gac agc gat ccg cat tat tta gag cgc 200  
 Gly Phe Thr Asp Leu Lys Leu Asp Ser Asp Pro His Tyr Leu Glu Arg  
 35 40 45 50  
 ttg aaa gcg ggc aaa atc tcg ccc cct aaa atc aaa gaa gaa aaa gaa 248  
 Leu Lys Ala Gly Lys Ile Ser Pro Pro Lys Ile Lys Glu Glu Lys Glu  
 55 60 65  
 acc tca aaa aac gcg aaa tta tcg tta tgg att ttt atc ggt ggg gtt 296  
 Thr Ser Lys Asn Ala Lys Leu Ser Leu Trp Ile Phe Ile Gly Gly Val  
 70 75 80  
 gta gcg atc gtt ttt tat gcg agc gcg att tct aaa aat atc gct ttt 344  
 Val Ala Ile Val Phe Tyr Ala Ser Ala Ile Ser Lys Asn Ile Ala Phe  
 85 90 95

gtt agc ccg gtg gtt tta ggc aga gat cac gcg att gtg tct ttc atg 392  
Val Ser Pro Val Val Leu Gly Arg Asp His Ala Ile Val Ser Phe Met  
100 105 110

cta agc gtg gcg act tta att gtg ctt ttt tgc aaa att aac gct aat 440  
Leu Ser Val Ala Thr Leu Ile Val Leu Phe Cys Lys Ile Asn Ala Asn  
115 120 125 130

gaa atc gct cat tca agc gtg ttt aaa tcc ggc atg caa gcg tgc gtg 488  
Glu Ile Ala His Ser Ser Val Phe Lys Ser Gly Met Gln Ala Cys Val  
135 140 145

tgc gtg ttg ggc gtg gcg tgg ttg ggc gat act ttt gtg agc aat cat 536  
Cys Val Leu Gly Val Ala Trp Leu Gly Asp Thr Phe Val Ser Asn His  
150 155 160

ata gat gag atc aaa cga tac gct tct ttt ttg atc gca gat tat ccg 584  
Ile Asp Glu Ile Lys Arg Tyr Ala Ser Phe Leu Ile Ala Asp Tyr Pro  
165 170 175

ttt tta tta gcc gta gcg ctc ttt ttg gct tcc atg ctt ttg tat tcg 632  
Phe Leu Leu Ala Val Ala Leu Phe Leu Ala Ser Met Leu Leu Tyr Ser  
180 185 190

caa gcc gcc acc tct aaa gcg ctc atc cca agc gtg atc aca gcc tta 680  
Gln Ala Ala Thr Ser Lys Ala Leu Ile Pro Ser Val Ile Thr Ala Leu  
195 200 205 210

ggc att agc gct aat cat acg gag cat ttg tat att atc gtg gct tcg 728  
Gly Ile Ser Ala Asn His Thr Glu His Leu Tyr Ile Ile Val Ala Ser  
215 220 225

ttt gcg agc gtt tcg gcg ttg ttt gtg tta ccc act tac ccc act tta 776  
Phe Ala Ser Val Ser Ala Leu Phe Val Leu Pro Thr Tyr Pro Thr Leu  
230 235 240

cta gga gcg atc gct atg gat aac acc ggc acc act aaa atg ggc cgt 824  
Leu Gly Ala Ile Ala Met Asp Asn Thr Gly Thr Thr Lys Met Gly Arg  
245 250 255

tat gtg ttt gat cat gcg ttt ttg atc cct ggg gtt tta gtc gtg tct 872  
Tyr Val Phe Asp His Ala Phe Leu Ile Pro Gly Val Leu Val Val Ser  
260 265 270

ttg agc gta gcg tta ggg ttt gtt gtc gcg ccg tta gtt ttg 914  
Leu Ser Val Ala Leu Gly Phe Val Val Ala Pro Leu Val Leu  
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<212> PRT  
<213> Helicobacter pylori

<400> 42  
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 Ile Met Gly Phe Thr Asp Leu Lys Leu Asp Ser Asp Pro His Tyr Leu  
 35 40 45  
 Glu Arg Leu Lys Ala Gly Lys Ile Ser Pro Pro Lys Ile Lys Glu Glu  
 50 55 60  
 Lys Glu Thr Ser Lys Asn Ala Lys Leu Ser Leu Trp Ile Phe Ile Gly  
 65 70 75 80  
 Gly Val Val Ala Ile Val Phe Tyr Ala Ser Ala Ile Ser Lys Asn Ile  
 85 90 95  
 Ala Phe Val Ser Pro Val Val Leu Gly Arg Asp His Ala Ile Val Ser  
 100 105 110  
 Phe Met Leu Ser Val Ala Thr Leu Ile Val Leu Phe Cys Lys Ile Asn  
 115 120 125  
 Ala Asn Glu Ile Ala His Ser Ser Val Phe Lys Ser Gly Met Gln Ala  
 130 135 140  
 Cys Val Cys Val Leu Gly Val Ala Trp Leu Gly Asp Thr Phe Val Ser  
 145 150 155 160  
 Asn His Ile Asp Glu Ile Lys Arg Tyr Ala Ser Phe Leu Ile Ala Asp  
 165 170 175  
 Tyr Pro Phe Leu Leu Ala Val Ala Leu Phe Leu Ala Ser Met Leu Leu  
 180 185 190  
 Tyr Ser Gln Ala Ala Thr Ser Lys Ala Leu Ile Pro Ser Val Ile Thr  
 195 200 205  
 Ala Leu Gly Ile Ser Ala Asn His Thr Glu His Leu Tyr Ile Ile Val  
 210 215 220  
 Ala Ser Phe Ala Ser Val Ser Ala Leu Phe Val Leu Pro Thr Tyr Pro  
 225 230 235 240  
 Thr Leu Leu Gly Ala Ile Ala Met Asp Asn Thr Gly Thr Thr Lys Met  
 245 250 255  
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 260 265 270  
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 Glu Asn Ser Ser Ile Trp Ser Asn Pro Ala Phe Val Ala Ile Ile Cys  
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 atg tgc gtt ctt agc ctt tta agg ctc aat gtc atg ctt tct atg att 152  
 Met Cys Val Leu Ser Leu Arg Leu Asn Val Met Leu Ser Met Ile  
 20 25 30  
 agt gcg act ctc ata gca gga ctt atg gga ggg ctt ggg atc acg gag 200  
 Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile Thr Glu

35	40										45					50					
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Ser Phe Asn Ala Met Ile Asp Gly Met Lys Gly Asn Leu Asn Ile Ala																					
55 60 65																					
tta agc tac atc ctt tta ggg gct tta gcg gta gcg atc gct aaa agc	296																				
Leu Ser Tyr Ile Leu Leu Gly Ala Leu Ala Val Ala Ile Ala Lys Ser																					
70 75 80																					
aat ctc att aaa gtc gct ttg agt aaa tta ata ggt tta atg gat tac	344																				
Asn Leu Ile Lys Val Ala Leu Ser Lys Leu Ile Gly Leu Met Asp Tyr																					
85 90 95																					
aag cga tcc act ttt tgc ttt ttg atc gct ttc atc gca tgc ttt tcg	392																				
Lys Arg Ser Thr Phe Cys Phe Leu Ile Ala Phe Ile Ala Cys Phe Ser																					
100 105 110																					
caa aat tta gtg ccg gtg cat atc gct ttt atc cct att tta atc ccc	440																				
Gln Asn Leu Val Pro Val His Ile Ala Phe Ile Pro Ile Leu Ile Pro																					
115 120 125 130																					
cct ctt ttg cat tta atg aac cgg cta gaa ttg gat aga aga gcg gtc	488																				
Pro Leu Leu His Leu Met Asn Arg Leu Glu Leu Asp Arg Arg Ala Val																					
135 140 145																					
gct tgc gct tta acc ttt ggc ttg caa gcc ccc tac ttg gtg ctt cct	536																				
Ala Cys Ala Leu Thr Phe Gly Leu Gln Ala Pro Tyr Leu Val Leu Pro																					
150 155 160																					
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Val Gly Phe Gly Leu Ile Phe Gln Thr Thr Ile Leu Glu Gln Leu Lys																					
165 170 175																					
gct aat ggc gtt agc acc acc ata gcg caa atc aca gga gtg atg tgg	632																				
Ala Asn Gly Val Ser Thr Thr Ile Ala Gln Ile Thr Gly Val Met Trp																					
180 185 190																					
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Ile Ala Gly Leu Ala Met Val Val Gly Leu Leu Val Ala Val Leu Thr																					
195 200 205 210																					
cta tac aaa aaa ccc agg cac tac aaa gag aaa tct ttt aat ata gaa	728																				
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230 235 240																					
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Gly Ile Val Val Ala Phe Val Ile Gln Leu Ala Thr Asp Ser Met Pro																					
245 250 255																					
tta gcc gcc ttt tta gcg tta gcg atc atc tta tta ggc cgt ggc att	872																				
Leu Ala Ala Phe Leu Ala Leu Ala Ile Ile Leu Leu Gly Arg Gly Ile																					
260 265 270																					
aag ttt aaa gaa aca gac tcg ctt atg gat gat agc gtg aaa atg atg	920																				



Met Trp Ile Ala Gly Leu Ala Met Val Val Gly Leu Leu Val Ala Val  
195 200 205  
Leu Thr Leu Tyr Lys Lys Pro Arg His Tyr Lys Glu Lys Ser Phe Asn  
210 215 220  
Ile Glu Asn Tyr Ala Ser Leu Gln Leu Asn Tyr His Asp Tyr Leu Thr  
225 230 235 240  
Phe Ile Gly Ile Val Val Ala Phe Val Ile Gln Leu Ala Thr Asp Ser  
245 250 255  
Met Pro Leu Ala Ala Phe Leu Ala Leu Ala Ile Ile Leu Leu Gly Arg  
260 265 270  
Gly Ile Lys Phe Lys Glu Thr Asp Ser Leu Met Asp Asp Ser Val Lys  
275 280 285  
Met Met Ala Phe Ile Ala Phe Val Met Leu Val Ala Ser Gly Phe Gly  
290 295 300  
Glu Val Leu Gln Lys Val His Ala Ile Glu Gly Leu Val Asn Ala Ile  
305 310 315 320  
Thr Ser Val Val Gln Gly Lys Leu Leu Gly Ala Phe Leu Met Leu Val  
325 330 335  
Val Gly Leu Phe Ile Thr Met Gly Ile Gly Thr Ser Phe Gly Thr Ile  
340 345 350  
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370 375

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<212> DNA  
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Val Gly Leu Val Thr Thr Leu Ala Leu Gly Ile Ser Cys Ile Ile  
1 5 10 15  
tta ttc gtg gcg ttt ttt agc atc att tgg cgg att ttg gct ttg att 156  
Leu Phe Val Ala Phe Phe Ser Ile Ile Trp Arg Ile Leu Ala Leu Ile  
20 25 30  
tct ggg ttc cct tct tgc tgt ttg tat tcg tcc tta act tct tgt tta 204  
Ser Gly Phe Pro Ser Cys Cys Leu Tyr Ser Ser Leu Thr Ser Cys Leu  
35 40 45  
gtc att ttt aaa gag ttg gtg tat tgg cgg cgt ttg atc gct aaa tct 252  
Val Ile Phe Lys Glu Leu Val Tyr Trp Arg Arg Leu Ile Ala Lys Ser  
50 55 60  
ata aaa gcc aag aca aaa aat aaa aat aaa agc gaa gaa atg agc cat 300  
Ile Lys Ala Lys Thr Lys Asn Lys Asn Lys Ser Glu Glu Met Ser His  
65 70 75 80  
aac gcc tta ttt tta aac cac aac aac tgg cct tgt aaa ttc aaa aga 348  
Asn Ala Leu Phe Leu Asn His Asn Asn Trp Pro Cys Lys Phe Lys Arg  
85 90 95



gcc gca tgg ttt aat tcc cct aaa aac aaa gaa aag atg aaa aac ccc 396  
 Ala Ala Trp Phe Asn Ser Pro Lys Asn Lys Glu Lys Met Lys Asn Pro  
 100 105 110

aga aaa aaa gct aaa aaa act ttt aag gtg atc aaa ctc cca tca agg 444  
 Arg Lys Lys Ala Lys Lys Thr Phe Lys Val Ile Lys Leu Pro Ser Arg  
 115 120 125

agc ttt ttt aaa gaa aaa agg ttt ttg acg cca ttg ata ggg ttg att 492  
 Ser Phe Phe Lys Glu Lys Arg Phe Leu Thr Pro Leu Ile Gly Leu Ile  
 130 135 140

tta gaa aat tta ggc tca atg act tta ggg gca aag agc cag cca aat 540  
 Leu Glu Asn Leu Gly Ser Met Thr Leu Gly Ala Lys Ser Gln Pro Asn  
 145 150 155 160

tgc aag aca tta gat aaa aac gcc acc acc act aaa atg att aaa atc 588  
 Cys Lys Thr Leu Asp Lys Asn Ala Thr Thr Thr Lys Met Ile Lys Ile  
 165 170 175

ggg aaa agc aat aaa aaa gtg tct tta gcc agt tgg tta aac agc tct 636  
 Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser  
 180 185 190

tgaacgcttt ctttactgaa atctagggaa aaatctttca acacatggcg atacatttcg 696  
 ctaaagccat ccaccacacca tataaaaaaa acaaaaatac taattagccc ggccaataac 756  
 cccaaaaccc ccaccacttc catgctctta ggcacattgc cttcttctct ggcttttttg 816  
 atttttttcg cgctagggag ttcgggtttt tcttcttcag ccattggccc tcttttttaa 876  
 aatttgaacg gctaattcat agtcttttag ggtgttttag tttaaaaatt cttcttcttt 936  
 gtcaaaatt 945

<210> 46  
 <211> 192  
 <212> PRT  
 <213> Helicobacter pylori

<400> 46  
 Val Gly Leu Val Thr Thr Thr Leu Ala Leu Gly Ile Ser Cys Ile Ile  
 1 5 10 15  
 Leu Phe Val Ala Phe Phe Ser Ile Ile Trp Arg Ile Leu Ala Leu Ile  
 20 25 30  
 Ser Gly Phe Pro Ser Cys Cys Leu Tyr Ser Ser Leu Thr Ser Cys Leu  
 35 40 45  
 Val Ile Phe Lys Glu Leu Val Tyr Trp Arg Arg Leu Ile Ala Lys Ser  
 50 55 60  
 Ile Lys Ala Lys Thr Lys Asn Lys Asn Lys Ser Glu Glu Met Ser His  
 65 70 75 80  
 Asn Ala Leu Phe Leu Asn His Asn Asn Trp Pro Cys Lys Phe Lys Arg  
 85 90 95  
 Ala Ala Trp Phe Asn Ser Pro Lys Asn Lys Glu Lys Met Lys Asn Pro  
 100 105 110  
 Arg Lys Lys Ala Lys Lys Thr Phe Lys Val Ile Lys Leu Pro Ser Arg  
 115 120 125  
 Ser Phe Phe Lys Glu Lys Arg Phe Leu Thr Pro Leu Ile Gly Leu Ile  
 130 135 140  
 Leu Glu Asn Leu Gly Ser Met Thr Leu Gly Ala Lys Ser Gln Pro Asn  
 145 150 155 160  
 Cys Lys Thr Leu Asp Lys Asn Ala Thr Thr Thr Lys Met Ile Lys Ile

Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser  
 165 170 175  
 180 185 190

<210> 47  
 <211> 851  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (49)...(783)

<400> 47  
 attgatagtt tcttcagcaa gaatgattag gcaatgatta gggttag atg aat ttt 57  
 Met Asn Phe  
 1  
 tat caa aaa ata tac act cat aaa gtc gtt ttt tct tca ttg ttt ttt 105  
 Tyr Gln Lys Ile Tyr Thr His Lys Val Val Phe Ser Ser Leu Phe Phe  
 5 10 15  
 ttg ttg ttt ttg ttc aat gtg gaa act ttg ttg ctt tcg cat ttc agc 153  
 Leu Leu Phe Leu Phe Asn Val Glu Thr Leu Leu Leu Ser His Phe Ser  
 20 25 30 35  
 gat gat ttt tcg caa ttg ttt ttt ttg ttt gaa aac cat gtt tat gat 201  
 Asp Asp Phe Ser Gln Leu Phe Phe Leu Phe Glu Asn His Val Tyr Asp  
 40 45 50  
 ttc att gtc aaa tta gat tat ttg ggg cta ata ggc gtt tct tta att 249  
 Phe Ile Val Lys Leu Asp Tyr Leu Gly Leu Ile Gly Val Ser Leu Ile  
 55 60 65  
 tat ctg ctt gtg ctt att cta aag cct ttc acc ctc acg cgc caa aaa 297  
 Tyr Leu Leu Val Leu Ile Leu Lys Pro Phe Thr Leu Thr Arg Gln Lys  
 70 75 80  
 tgc gct tgc gta ggg ata tta tgc ctt tct ttc tac gct tgg aat ttt 345  
 Cys Ala Cys Val Gly Ile Leu Cys Leu Ser Phe Tyr Ala Trp Asn Phe  
 85 90 95  
 cct gtt aaa gat tct tta atg gtg ctt tat ctt ttc tat ttt gcg ctg 393  
 Pro Val Lys Asp Ser Leu Met Val Leu Tyr Leu Phe Tyr Phe Ala Leu  
 100 105 110 115  
 tta gcg act tta ttg tgg cgt ttt tta ggg gct agc atg aag caa tct 441  
 Leu Ala Thr Leu Leu Trp Arg Phe Leu Gly Ala Ser Met Lys Gln Ser  
 120 125 130  
 ttc ttg ccc tct atg aat att tgc atc gtg tgg gtt ttt gct tct tct 489  
 Phe Leu Pro Ser Met Asn Ile Cys Ile Val Trp Val Phe Ala Ser Ser  
 135 140 145  
 tta cag agt ttt agg ttt tta agc gtg tct gat tgc gtg gat ttt tcc 537  
 Leu Gln Ser Phe Arg Phe Leu Ser Val Ser Asp Cys Val Asp Phe Ser  
 150 155 160  
 ctt ttt aca ctc gcg ctt att tta ttg ata ctg gtt tta atc tat tgc 585



Gly Leu Leu Gly Trp Leu Leu Glu Tyr Val His Asn Thr Leu Arg Arg  
 225 230 235 240  
 Leu Glu His Gln Ile  
 245

<210> 49  
 <211> 827  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (95)...(745)

<400> 49  
 ctttttacttt ttagttaagt tgtaagaaac ttttagctacc atgcgataca aaaaaggatt 60  
 ttaagtgcgt tttggtaaaa ttgattattt gaac atg ctc cct ttt gat gtg ttt 115  
 Met Leu Pro Phe Asp Val Phe  
 1 5

atc aaa tcc tac ccc acc cct tgt tat ttc aaa caa ttc tta cgg ctt 163  
 Ile Lys Ser Tyr Pro Thr Pro Cys Tyr Phe Lys Gln Phe Leu Arg Leu  
 10 15 20

aaa aaa acc tac ccc tcc aaa ctc aat gag agt ttt tta ttc agg cgt 211  
 Lys Lys Thr Tyr Pro Ser Lys Leu Asn Glu Ser Phe Leu Phe Arg Arg  
 25 30 35

att gat gcg ggg ttt att tct tct atc gcc ggc tat cca ttc gct ctt 259  
 Ile Asp Ala Gly Phe Ile Ser Ser Ile Ala Gly Tyr Pro Phe Ala Leu  
 40 45 50 55

cat tcc cat tct cta ggc att gtc gct tat aag gaa gtt tta agc gtg 307  
 His Ser His Ser Leu Gly Ile Val Ala Tyr Lys Glu Val Leu Ser Val  
 60 65 70

ctg gtt gtg gat aca aaa aac gct ttt gat aaa gaa agc gct tct tca 355  
 Leu Val Val Asp Thr Lys Asn Ala Phe Asp Lys Glu Ser Ala Ser Ser  
 75 80 85

aac gcc ctc tct caa gcg cta ggg tta aag ggc gaa gtg tta atc ggc 403  
 Asn Ala Leu Ser Gln Ala Leu Gly Leu Lys Gly Glu Val Leu Ile Gly  
 90 95 100

aat aaa gca ctg cag ttt tat tat tcc aac cct aaa aaa gat ttt ata 451  
 Asn Lys Ala Leu Gln Phe Tyr Tyr Ser Asn Pro Lys Lys Asp Phe Ile  
 105 110 115

gat tta gcc gct ctt tgg tat gaa aaa aaa cgc ttg ccg ttt gtt ttt 499  
 Asp Leu Ala Ala Leu Trp Tyr Glu Lys Lys Arg Leu Pro Phe Val Phe  
 120 125 130 135

ggg cgt ttg tgt tat tac caa aac aag gat ttt tac aag cgc ttg tct 547  
 Gly Arg Leu Cys Tyr Tyr Gln Asn Lys Asp Phe Tyr Lys Arg Leu Ser  
 140 145 150

tta gct ttc aaa cat caa aaa aca aaa atc cct tac tac atc ctt aaa 595  
 Leu Ala Phe Lys His Gln Lys Thr Lys Ile Pro Tyr Tyr Ile Leu Lys  
 155 160 165



<220>  
 <221> CDS  
 <222> (76)...(663)

<400> 51

gcaacaagaa atttttagaga aaatgagacc caacgctcaa aaaattcaag cgggttaaac	60
ggctaaaaag gagag atg atg gga tac att cct tat gta ata gag aat acc	111
Met Met Gly Tyr Ile Pro Tyr Val Ile Glu Asn Thr	
1 5 10	
gat cgt ggg gag cgt agc tat gat att tac tcg cgc ctt tta aag gat	159
Asp Arg Gly Glu Arg Ser Tyr Asp Ile Tyr Ser Arg Leu Leu Lys Asp	
15 20 25	
cgc att gtt tta ttg agc ggt gaa att aat gac agc gtg gcg tct tct	207
Arg Ile Val Leu Leu Ser Gly Glu Ile Asn Asp Ser Val Ala Ser Ser	
30 35 40	
atc gtg gcc caa ctc ttg ttt ttg gaa gct gaa gac cct gaa aaa gac	255
Ile Val Ala Gln Leu Leu Phe Leu Glu Ala Glu Asp Pro Glu Lys Asp	
45 50 55 60	
att ggt ttg tat atc aat tct ccc ggt ggg gtg ata aca agc ggt ctt	303
Ile Gly Leu Tyr Ile Asn Ser Pro Gly Gly Val Ile Thr Ser Gly Leu	
65 70 75	
agt att tat gac acc atg aat ttt atc cgc cct gat gtt tcc acg att	351
Ser Ile Tyr Asp Thr Met Asn Phe Ile Arg Pro Asp Val Ser Thr Ile	
80 85 90	
tgc atc ggt caa gcg gct tct atg ggg gcg ttt tta ctg agc tgt ggg	399
Cys Ile Gly Gln Ala Ala Ser Met Gly Ala Phe Leu Leu Ser Cys Gly	
95 100 105	
gct aag ggc aag cgc ttt tcg cta ccc cat tca agg att atg atc cac	447
Ala Lys Gly Lys Arg Phe Ser Leu Pro His Ser Arg Ile Met Ile His	
110 115 120	
cag cct tta ggg ggg gct caa ggg caa gcg agc gat att gaa atc att	495
Gln Pro Leu Gly Gly Ala Gln Gly Gln Ala Ser Asp Ile Glu Ile Ile	
125 130 135 140	
tct aat gag att ctc agg ctt aaa ggc ttg atg aat tct att cta gct	543
Ser Asn Glu Ile Leu Arg Leu Lys Gly Leu Met Asn Ser Ile Leu Ala	
145 150 155	
caa aac tca ggg cag agt ttg gag caa atc gct aaa gac acg gac agg	591
Gln Asn Ser Gly Gln Ser Leu Glu Gln Ile Ala Lys Asp Thr Asp Arg	
160 165 170	
gat ttt tat atg agt gct aaa gaa gct aaa gag tat ggc ttg att gat	639
Asp Phe Tyr Met Ser Ala Lys Glu Ala Lys Glu Tyr Gly Leu Ile Asp	
175 180 185	
aaa gtg tta cag aaa aac gtg aag tgattgcatg gcgttattag agattatcca	693
Lys Val Leu Gln Lys Asn Val Lys	
190 195	
ttacccttct aaaatcttaa gaacgatttc taaagaggtc gtt	736

<210> 52  
 <211> 196  
 <212> PRT  
 <213> Helicobacter pylori

<400> 52  
 Met Met Gly Tyr Ile Pro Tyr Val Ile Glu Asn Thr Asp Arg Gly Glu  
 1 5 10 15  
 Arg Ser Tyr Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Val Leu  
 20 25 30  
 Leu Ser Gly Glu Ile Asn Asp Ser Val Ala Ser Ser Ile Val Ala Gln  
 35 40 45  
 Leu Leu Phe Leu Glu Ala Glu Asp Pro Glu Lys Asp Ile Gly Leu Tyr  
 50 55 60  
 Ile Asn Ser Pro Gly Gly Val Ile Thr Ser Gly Leu Ser Ile Tyr Asp  
 65 70 75 80  
 Thr Met Asn Phe Ile Arg Pro Asp Val Ser Thr Ile Cys Ile Gly Gln  
 85 90 95  
 Ala Ala Ser Met Gly Ala Phe Leu Leu Ser Cys Gly Ala Lys Gly Lys  
 100 105 110  
 Arg Phe Ser Leu Pro His Ser Arg Ile Met Ile His Gln Pro Leu Gly  
 115 120 125  
 Gly Ala Gln Gly Gln Ala Ser Asp Ile Glu Ile Ile Ser Asn Glu Ile  
 130 135 140  
 Leu Arg Leu Lys Gly Leu Met Asn Ser Ile Leu Ala Gln Asn Ser Gly  
 145 150 155 160  
 Gln Ser Leu Glu Gln Ile Ala Lys Asp Thr Asp Arg Asp Phe Tyr Met  
 165 170 175  
 Ser Ala Lys Glu Ala Lys Glu Tyr Gly Leu Ile Asp Lys Val Leu Gln  
 180 185 190  
 Lys Asn Val Lys  
 195

<210> 53  
 <211> 904  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)...(852)

<400> 53  
 cgc ata aaa aaa gaa cgc ttg aac aaa ctg ctt aaa agg ggg ttt tta 48  
 Arg Ile Lys Lys Glu Arg Leu Asn Lys Leu Leu Lys Arg Gly Phe Leu  
 1 5 10 15  
 gcg ttc ttt ttg agc gtg tat tta agg gct gat gat ttg gtt act tac 96  
 Ala Phe Phe Leu Ser Val Tyr Leu Arg Ala Asp Asp Leu Val Thr Tyr  
 20 25 30  
 acc atc atc aaa gaa aaa gat cta gga tac cag cgg ttt tta gcc aag 144  
 Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys  
 35 40 45  
 aag tgt tta agg ggt aaa acc cac cct ccg tgt ttt act aag cct aaa 192  
 Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys  
 50 55 60

aag cct aaa aga aaa ctt ttt aat ata gac aaa agc tcc cac tat tat	240
Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr	
65 70 75 80	
ggc aca agc gtg gtg caa atg tca tgg cta cag agt agg gaa aaa ttt	288
Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe	
85 90 95	
gaa aac cat tca aaa tac cga gac att cct ttt gct gaa gtc agt ttg	336
Glu Asn His Ser Lys Tyr Arg Asp Ile Pro Phe Ala Glu Val Ser Leu	
100 105 110	
att tat ggc tat aaa caa ttt ttt cct aaa aaa gag cgc tac ggc ttc	384
Ile Tyr Gly Tyr Lys Gln Phe Phe Pro Lys Lys Glu Arg Tyr Gly Phe	
115 120 125	
cgt ttt tat gtc tct ttg gat tac gct tat ggg ttt ttt ctt aaa aat	432
Arg Phe Tyr Val Ser Leu Asp Tyr Ala Tyr Gly Phe Phe Leu Lys Asn	
130 135 140	
aag ggc gtg ttg ggc gat agt ttg agg gag agt tcg caa atc cct aaa	480
Lys Gly Val Leu Gly Asp Ser Leu Arg Glu Ser Ser Gln Ile Pro Lys	
145 150 155 160	
agc tat aga gaa aaa ttg caa aga aaa gag act ttt att aac gct att	528
Ser Tyr Arg Glu Lys Leu Gln Arg Lys Glu Thr Phe Ile Asn Ala Ile	
165 170 175	
ttt tat ggc gcg gga gct gac ttt tta tac aaa cgc gct ttt gga acg	576
Phe Tyr Gly Ala Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly Thr	
180 185 190	
ctg att tta ggg atg aat ttc gtg gga gaa acc tgg ttt tat gaa aca	624
Leu Ile Leu Gly Met Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu Thr	
195 200 205	
aag att ttt aaa aag tgg gct aaa gat cct ttg agc gtt tat cac cct	672
Lys Ile Phe Lys Lys Trp Ala Lys Asp Pro Leu Ser Val Tyr His Pro	
210 215 220	
tac atg ttt caa gtg atg ttg aat gtg ggg tat cgt tac cgc ttt tca	720
Tyr Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe Ser	
225 230 235 240	
agg tat aag aat tgg gcg ata gaa ttg ggt gcg cgc atc cct ttt tta	768
Arg Tyr Lys Asn Trp Ala Ile Glu Leu Gly Ala Arg Ile Pro Phe Leu	
245 250 255	
acc aat gat tat ttt aaa acc cct tta tac acc ctt cat ttc aag cgc	816
Thr Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys Arg	
260 265 270	
aat att tct gtc tat ctc act tca act tat gac ttt tagtttttta	862
Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe	
275 280	
aattttttgaa aactagaatt aaaaccgctt tttataaact gg	904

<210> 54



<211> 284  
 <212> PRT  
 <213> Helicobacter pylori

<400> 54

Arg	Ile	Lys	Lys	Glu	Arg	Leu	Asn	Lys	Leu	Leu	Lys	Arg	Gly	Phe	Leu
1				5					10					15	
Ala	Phe	Phe	Leu	Ser	Val	Tyr	Leu	Arg	Ala	Asp	Asp	Leu	Val	Thr	Tyr
			20					25					30		
Thr	Ile	Ile	Lys	Glu	Lys	Asp	Leu	Gly	Tyr	Gln	Arg	Phe	Leu	Ala	Lys
		35					40					45			
Lys	Cys	Leu	Arg	Gly	Lys	Thr	His	Pro	Pro	Cys	Phe	Thr	Lys	Pro	Lys
	50					55					60				
Lys	Pro	Lys	Arg	Lys	Leu	Phe	Asn	Ile	Asp	Lys	Ser	Ser	His	Tyr	Tyr
65					70				75						80
Gly	Thr	Ser	Val	Val	Gln	Met	Ser	Trp	Leu	Gln	Ser	Arg	Glu	Lys	Phe
				85					90					95	
Glu	Asn	His	Ser	Lys	Tyr	Arg	Asp	Ile	Pro	Phe	Ala	Glu	Val	Ser	Leu
			100					105					110		
Ile	Tyr	Gly	Tyr	Lys	Gln	Phe	Phe	Pro	Lys	Lys	Glu	Arg	Tyr	Gly	Phe
		115					120					125			
Arg	Phe	Tyr	Val	Ser	Leu	Asp	Tyr	Ala	Tyr	Gly	Phe	Phe	Leu	Lys	Asn
		130				135					140				
Lys	Gly	Val	Leu	Gly	Asp	Ser	Leu	Arg	Glu	Ser	Ser	Gln	Ile	Pro	Lys
145					150				155						160
Ser	Tyr	Arg	Glu	Lys	Leu	Gln	Arg	Lys	Glu	Thr	Phe	Ile	Asn	Ala	Ile
				165					170					175	
Phe	Tyr	Gly	Ala	Gly	Ala	Asp	Phe	Leu	Tyr	Lys	Arg	Ala	Phe	Gly	Thr
			180					185					190		
Leu	Ile	Leu	Gly	Met	Asn	Phe	Val	Gly	Glu	Thr	Trp	Phe	Tyr	Glu	Thr
		195					200					205			
Lys	Ile	Phe	Lys	Lys	Trp	Ala	Lys	Asp	Pro	Leu	Ser	Val	Tyr	His	Pro
	210					215					220				
Tyr	Met	Phe	Gln	Val	Met	Leu	Asn	Val	Gly	Tyr	Arg	Tyr	Arg	Phe	Ser
225					230				235						240
Arg	Tyr	Lys	Asn	Trp	Ala	Ile	Glu	Leu	Gly	Ala	Arg	Ile	Pro	Phe	Leu
				245					250					255	
Thr	Asn	Asp	Tyr	Phe	Lys	Thr	Pro	Leu	Tyr	Thr	Leu	His	Phe	Lys	Arg
			260					265					270		
Asn	Ile	Ser	Val	Tyr	Leu	Thr	Ser	Thr	Tyr	Asp	Phe				
		275					280								

<210> 55  
 <211> 1172  
 <212> DNA  
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (75)...(1106)

<400> 55

taatcggttat	taa	catgct	at	at	ttt	cttt	ttt	ctata	aaa	act	caatatt	att	gaata	aaa	60
actagggagt	taga	atg	atc	tta	aaa	cga	gtt	act	gaa	gct	tta	gaa	gcg		110
		Met	Ile	Leu	Lys	Arg	Val	Thr	Glu	Ala	Leu	Glu	Ala		
		1				5					10				
tat	aaa	aat	ggc	gaa	atg	ctc	att	gtt	atg	gac	gat	gaa	gac	aga	gaa
Tyr	Lys	Asn	Gly	Glu	Met	Leu	Ile	Val	Met	Asp	Asp	Glu	Asp	Arg	Glu

158

15	20	25	
aat gag ggg gat ttg gtt tta gct ggg att ttt tct acc cct gag aaa Asn Glu Gly Asp Leu Val Leu Ala Gly Ile Phe Ser Thr Pro Glu Lys 30 35 40			206
atc aat ttc atg gcc acg cat gct agg ggg ttg att tgc gtg tct ttg Ile Asn Phe Met Ala Thr His Ala Arg Gly Leu Ile Cys Val Ser Leu 45 50 55 60			254
acc aaa gat tta gcg aaa aaa ttt gaa tta ccc cct atg gtt agc gtg Thr Lys Asp Leu Ala Lys Lys Phe Glu Leu Pro Pro Met Val Ser Val 65 70 75			302
aat gat tct aac cat gag acc gct ttc acg gtt tcc att gac gct aaa Asn Asp Ser Asn His Glu Thr Ala Phe Thr Val Ser Ile Asp Ala Lys 80 85 90			350
gaa gcc aga acc ggg att tct gct ttt gaa agg cat tta acg att gaa Glu Ala Arg Thr Gly Ile Ser Ala Phe Glu Arg His Leu Thr Ile Glu 95 100 105			398
tta ttg tgt aaa gac acc acc aaa ccg agc gat ttt gtg cgc ccg ggg Leu Leu Cys Lys Asp Thr Thr Lys Pro Ser Asp Phe Val Arg Pro Gly 110 115 120			446
cat att ttc cct ttg atc gcc aaa gac ggg ggc gtg tta gcg cgc acg His Ile Phe Pro Leu Ile Ala Lys Asp Gly Gly Val Leu Ala Arg Thr 125 130 135 140			494
ggc cat act gaa gcg agc gtg gat ttg tgc aaa tta gct gga tta aag Gly His Thr Glu Ala Ser Val Asp Leu Cys Lys Leu Ala Gly Leu Lys 145 150 155			542
ccc gtg agc gtg att tgt gaa atc atg aaa gaa gat ggc tct atg gcg Pro Val Ser Val Ile Cys Glu Ile Met Lys Glu Asp Gly Ser Met Ala 160 165 170			590
aga agg ggg gat aaa ttt ttg agc gat ttc gcc ctc aaa cat aac ctt Arg Arg Gly Asp Lys Phe Leu Ser Asp Phe Ala Leu Lys His Asn Leu 175 180 185			638
aaa act ctc tat gtc tct gat ttg att agc tat cgt ttg gaa aat gaa Lys Thr Leu Tyr Val Ser Asp Leu Ile Ser Tyr Arg Leu Glu Asn Glu 190 195 200			686
agt ttg ctg aaa atg ttt tgt caa gaa gaa agg gaa ttt tta aaa cac Ser Leu Leu Lys Met Phe Cys Gln Glu Glu Arg Glu Phe Leu Lys His 205 210 215 220			734
caa acg caa tgc tac act ttt tta gat cac cag caa aaa aac cat tac Gln Thr Gln Cys Tyr Thr Phe Leu Asp His Gln Gln Lys Asn His Tyr 225 230 235			782
gct ttt aag ttt aaa ggc gca aaa acc cat gat tta gcc cct tta gtg Ala Phe Lys Phe Lys Gly Ala Lys Thr His Asp Leu Ala Pro Leu Val 240 245 250			830
cgt ttc cac cct atc aaa gag gat ttt gat ttt tta acg act gat gcg			878



Tyr	Thr	Phe	Leu	Asp	His	Gln	Gln	Lys	Asn	His	Tyr	Ala	Phe	Lys	Phe
225					230					235					240
Lys	Gly	Ala	Lys	Thr	His	Asp	Leu	Ala	Pro	Leu	Val	Arg	Phe	His	Pro
				245					250					255	
Ile	Lys	Glu	Asp	Phe	Asp	Phe	Leu	Thr	Thr	Asp	Ala	Phe	Glu	Val	Phe
			260					265					270		
Phe	Lys	Ala	Leu	Glu	Tyr	Leu	Lys	His	Glu	Gly	Gly	Tyr	Leu	Ile	Phe
		275					280					285			
Met	Asn	Thr	His	Ser	Lys	Glu	Asn	Asn	Val	Val	Lys	Asp	Phe	Gly	Ile
	290					295					300				
Gly	Ala	Leu	Val	Leu	Lys	Asn	Leu	Gly	Ile	Lys	Asp	Phe	Arg	Leu	Leu
305					310					315					320
Ser	Ser	Cys	Glu	Asp	Arg	Gln	Tyr	Lys	Ala	Leu	Ser	Gly	Phe	Gly	Leu
				325					330					335	
Lys	Leu	Val	Glu	Thr	Ile	Ser	Leu								
			340												

<210> 57  
 <211> 394  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(341)

<400> 57 gattttatcct tgcataaaac aatctcgctt ggcgataaaa aacgctctaa aaa ctt <div style="text-align: right;">Lys Leu</div> <div style="text-align: right;">1</div>															56
cat ttt aaa gcg ttt cac gca ctt ttc tat cct agc aat aga gac aat <div style="text-align: right;">Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg Asp Asn</div> <div style="text-align: right;">5 10 15</div>															104
atc tat gcc aat cat tta aaa tta ttg gat aat gaa atc agt gaa aaa <div style="text-align: right;">Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser Glu Lys</div> <div style="text-align: right;">20 25 30</div>															152
gac att ttt aat aaa gcc atc aat caa aaa cga att caa atg gct ctt <div style="text-align: right;">Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met Ala Leu</div> <div style="text-align: right;">35 40 45 50</div>															200
aat ctc atc ttt aag ctt gtt ttt gcc ttt gtt agt aac cac ttc ttc <div style="text-align: right;">Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His Phe Phe</div> <div style="text-align: right;">55 60 65</div>															248
cac gct ttt aga cga cag aat ctc tat aat cgt gtc ttt aat cgc tgt <div style="text-align: right;">His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn Arg Cys</div> <div style="text-align: right;">70 75 80</div>															296
gtc ttt aac ctt gac ttc att caa aag ctt ttc att act caa ttc <div style="text-align: right;">Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln Phe</div> <div style="text-align: right;">85 90 95</div>															341
taacgaaata gaagccttaa ggtagcgtct gccattttga gagaccagat tca															394

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<212> PRT  
 <213> Helicobacter pylori

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 20 25 30  
 Glu Lys Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met  
 35 40 45  
 Ala Leu Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His  
 50 55 60  
 Phe Phe His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn  
 65 70 75 80  
 Arg Cys Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln  
 85 90 95  
 Phe

<210> 59  
 <211> 360  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 agactttttt tgaatgagta a gga gaa aat att ttg ttc cat aaa ctg atc 111  
 Gly Glu Asn Ile Leu Phe His Lys Leu Ile  
 1 5 10  
 tta aca tgc ttt tta gcg ctt gta gca ata acc att caa gct tgc ggt 159  
 Leu Thr Cys Phe Leu Ala Leu Val Ala Ile Thr Ile Gln Ala Cys Gly  
 15 20 25  
 tat aaa gcc cct cca ttc aat gaa aaa ccc gct aaa aaa act tca aac 207  
 Tyr Lys Ala Pro Pro Phe Asn Glu Lys Pro Ala Lys Lys Thr Ser Asn  
 30 35 40  
 agc tct aat tct tct atg caa acg ccc acc aac agc acc acg cca gaa 255  
 Ser Ser Asn Ser Ser Met Gln Thr Pro Thr Asn Ser Thr Thr Pro Glu  
 45 50 55  
 ttt tta aat cag cct taaaatcact gctcttggtt aagggttttg atttctaggg 310  
 Phe Leu Asn Gln Pro  
 60  
 tttttgtggc taacttttga nsttcgcttt catcatgcgt taccataatg 360

<210> 60  
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 <212> PRT  
 <213> Helicobacter pylori

<400> 60  
 Gly Glu Asn Ile Leu Phe His Lys Leu Ile Leu Thr Cys Phe Leu Ala

[illegible]

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           5                  10                  15

gct tgc gga ttt tta aaa tcg tta ggt ttt gaa atg gtg gag agg aac 152  
Ala Cys Gly Phe Leu Lys Ser Leu Gly Phe Glu Met Val Glu Arg Asn  
20 25 30

ttt ttt tca caa ttt ggc gaa att gat att atc gct ttg aaa aaa ggg 200  
Phe Phe Ser Gln Phe Gly Glu Ile Asp Ile Ile Ala Leu Lys Lys Gly  
35 40 45 50

ggt ttg cat ttc att gaa gtc aaa agc ggg gaa aat ttt gat ccc att 248  
Val Leu His Phe Ile Glu Val Lys Ser Gly Glu Asn Phe Asp Pro Ile  
55 60 65

tat gcg atc acg ccg agc aaa tta aaa aag atg att aaa acg atc cgc 296  
Tyr Ala Ile Thr Pro Ser Lys Leu Lys Lys Met Ile Lys Thr Ile Arg  
70 75 80

tgt tat ttg tcc caa aaa gat ccc aat agc gat ttt tgc ata gac gct      344  
 Cys Tyr Leu Ser Gln Lys Asp Pro Asn Ser Asp Phe Cys Ile Asp Ala  
           85                          90                          95

ctt att gtg aaa aat ggt aaa ttt gag ctt tta gaa aat atc act ttt 392  
Leu Ile Val Lys Asn Gly Lys Phe Glu Leu Leu Glu Asn Ile Thr Phe  
100 105 110

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Phe Glu Gly Ile Arg Val Gln Gly Phe Phe Lys Tyr Phe Ala His Phe	
125 130 135	
gca ggt cct gtg aaa tgg ctc gcc cct ttc atg ttc cct att gag atc	544
Ala Gly Pro Val Lys Trp Leu Ala Pro Phe Met Phe Pro Ile Glu Ile	
140 145 150	
atc tcg cat ttt tct agg atc gtg tct tta tcg ttt cgt ttg ttt ggg	592
Ile Ser His Phe Ser Arg Ile Val Ser Leu Ser Phe Arg Leu Phe Gly	
155 160 165	
aat atc aag ggc gat gac atg ttc ttg ctc atc atg ctt tta tta gtg	640
Asn Ile Lys Gly Asp Asp Met Phe Leu Leu Ile Met Leu Leu Leu Val	
170 175 180 185	
cct tgg gcg gtt cct gta gcg cct ttt atg gtg ttg ttt ttc atg ggg	688
Pro Trp Ala Val Pro Val Ala Pro Phe Met Val Leu Phe Phe Met Gly	
190 195 200	
att tta caa gct ttt gtt ttt atg atc ctc act tat gtg tat ttg gca	736
Ile Leu Gln Ala Phe Val Phe Met Ile Leu Thr Tyr Val Tyr Leu Ala	
205 210 215	
ggg gct gtt tta acc gat gaa ggg cat taagcaataa cattcttggt	783
Gly Ala Val Leu Thr Asp Glu Gly His	
220 225	
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<212> PRT	
<213> Helicobacter pylori	
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Leu Ile Ser Leu Gly Ala Ser Arg Lys Met Gln Met Val Pro Met Gly	
35 40 45	
Leu Gln Asn Val Tyr Glu Ser Ile Ile Ser Ala Ile Leu Ser Val Ala	
50 55 60	
Lys Asp Ile Ile Gly Glu Glu Leu Ala Arg Lys Tyr Phe Pro Leu Ala	
65 70 75 80	
Gly Thr Ile Ala Leu Tyr Val Phe Phe Ser Asn Met Ile Gly Ile Ile	
85 90 95	
Pro Gly Phe Glu Ser Pro Thr Ala Ser Trp Ser Phe Thr Leu Val Leu	
100 105 110	
Ala Leu Ile Val Phe Phe Tyr Tyr His Phe Glu Gly Ile Arg Val Gln	
115 120 125	
Gly Phe Phe Lys Tyr Phe Ala His Phe Ala Gly Pro Val Lys Trp Leu	
130 135 140	
Ala Pro Phe Met Phe Pro Ile Glu Ile Ile Ser His Phe Ser Arg Ile	
145 150 155 160	
Val Ser Leu Ser Phe Arg Leu Phe Gly Asn Ile Lys Gly Asp Asp Met	
165 170 175	
Phe Leu Leu Ile Met Leu Leu Leu Val Pro Trp Ala Val Pro Val Ala	





Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser	Asn	His		
			150					155					160				
att	att	tta	gac	acc	aaa	aac	gcc	ctt	tta	gca	tgc	gac	act	aaa	ggc		584
Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr	Lys	Gly		
		165					170					175					
gat	ggg	gcg	atg	gct	gag	cct	tta	gaa	atc	ctt	ttt	aaa	gcc	gct	caa		632
Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala	Ala	Gln		
	180					185					190						
acg	ctc	cta	aaa	gac	gct	tat	ttt	gaa	aac	aga	gaa	gtc	ata	gtc	atg		680
Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile	Val	Met		
	195				200					205					210		
ggc	ggc	gcg	agt	ata	gaa	aag	att	gac	agc	gtt	cga	acg	att	agc	aat		728
Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile	Ser	Asn		
				215				220						225			
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Thr	Phe																

cca

787

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 <212> PRT  
 <213> Helicobacter pylori

<400> 66

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		20						25					30				
Leu	Glu	Leu	Val	Arg	Leu	Leu	Phe	Lys	Ser	Gly	Ala	Ser	Ile	Gln	Val		
		35					40					45					
Val	Met	Ser	Lys	Gly	Ala	Lys	Phe	Ile	Lys	Pro	Leu	Ser	Phe	Glu			
	50					55				60							
Ala	Leu	Ser	His	His	Lys	Val	Leu	His	Asp	Arg	Asn	Glu	Lys	Trp	Tyr		
	65				70				75					80			
Tyr	Asn	His	Gln	Asn	Ala	Leu	His	His	Asn	His	Ile	Ala	Cys	Ala	Ala		
			85					90					95				
Asn	Ala	Asp	Leu	Leu	Ile	Phe	Ala	Pro	Leu	Ser	Thr	Asn	Ser	Leu	Ser		
		100					105					110					
Lys	Ile	Ala	His	Ala	Leu	Ala	Asp	Asn	Ile	Val	Ser	Ala	Thr	Phe	Leu		
		115					120					125					
Ala	Cys	Ala	Ser	Pro	Lys	Ile	Leu	Ala	Pro	Ser	Met	Asn	Thr	Asn	Met		
	130					135					140						
Leu	Asn	Ser	Pro	Ile	Thr	Gln	Ser	Asn	Leu	Lys	Arg	Leu	Lys	Asp	Ser		
	145				150					155				160			
Asn	His	Ile	Ile	Leu	Asp	Thr	Lys	Asn	Ala	Leu	Leu	Ala	Cys	Asp	Thr		
			165				170						175				
Lys	Gly	Asp	Gly	Ala	Met	Ala	Glu	Pro	Leu	Glu	Ile	Leu	Phe	Lys	Ala		
		180					185					190					
Ala	Gln	Thr	Leu	Leu	Lys	Asp	Ala	Tyr	Phe	Glu	Asn	Arg	Glu	Val	Ile		
		195				200					205						
Val	Met	Gly	Gly	Ala	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Arg	Thr	Ile		
	210					215					220						

105230 "E" 55555

Ser Asn Thr Phe  
225

<210> 67  
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<212> DNA  
<213> Helicobacter pylori

<220>  
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<222> (71)...(1009)

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Met Lys Pro Gln Asp Ile Glu Ile Val Gln Ser Val Leu  
1 5 10  
  
gag att aca gga ccg att aag cct act gaa gtg tat gat aaa gcc aaa 157  
Glu Ile Thr Gly Pro Ile Lys Pro Thr Glu Val Tyr Asp Lys Ala Lys  
15 20 25  
  
gag ctt ttt gaa aaa ggt gag att aca aac atg ttt gat tgt ggg ggc 205  
Glu Leu Phe Glu Lys Gly Glu Ile Thr Asn Met Phe Asp Cys Gly Gly  
30 35 40 45  
  
aaa acc ccg cac cag agc gtt agt tct tat att tat aca gcc tta aac 253  
Lys Thr Pro His Gln Ser Val Ser Ser Tyr Ile Tyr Thr Ala Leu Asn  
50 55 60  
  
aag ggc gaa gaa ctg cct ttt aaa aaa gtg caa gaa aac cca acc tta 301  
Lys Gly Glu Glu Leu Pro Phe Lys Lys Val Gln Glu Asn Pro Thr Leu  
65 70 75  
  
atc gct tta aaa gac gcg gct aaa gag cta ggt tta gac gct caa aaa 349  
Ile Ala Leu Lys Asp Ala Ala Lys Glu Leu Gly Leu Asp Ala Gln Lys  
80 85 90  
  
ata agc gct cca agc tct aaa atc gcg cat gaa agg gat ttg cac ccc 397  
Ile Ser Ala Pro Ser Ser Lys Ile Ala His Glu Arg Asp Leu His Pro  
95 100 105  
  
ttt tta acc tac atg gct att aat aac gaa aat ttg aaa tgc tac acg 445  
Phe Leu Thr Tyr Met Ala Ile Asn Asn Glu Asn Leu Lys Cys Tyr Thr  
110 115 120 125  
  
aaa acc att ttt cat gaa gag agt tca aaa tca ata aaa ggc atg gac 493  
Lys Thr Ile Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp  
130 135 140  
  
agg tgg ctt tat ccg gac atg gtg ggg gtt agg ttt ttg cac gct gaa 541  
Arg Trp Leu Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu  
145 150 155  
  
tta tct aat gaa aat tta atc gct ttt tct aag aaa ttt gac act tta 589  
Leu Ser Asn Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu  
160 165 170  
  
ccc att aaa ctg gtg agc ttt gaa ttg aaa aaa gaa atc agc gtg cat 637



Phe His Glu Glu Ser Ser Lys Ser Ile Lys Gly Met Asp Arg Trp Leu  
 130 135 140  
 Tyr Pro Asp Met Val Gly Val Arg Phe Leu His Ala Glu Leu Ser Asn  
 145 150 155 160  
 Glu Asn Leu Ile Ala Phe Ser Lys Lys Phe Asp Thr Leu Pro Ile Lys  
 165 170 175  
 Leu Val Ser Phe Glu Leu Lys Lys Glu Ile Ser Val His Asn Cys Arg  
 180 185 190  
 Glu Cys Tyr Phe Gln Ala Ile Ser Asn Ser Ser Trp Ala Asn Glu Gly  
 195 200 205  
 Tyr Leu Val Gly Arg His Ile Asp Thr His Asn Pro Gln Leu Met Asp  
 210 215 220  
 Leu Leu Lys Arg Leu His Ala Ser Phe Gly Ile Gly Val Ile Asp Leu  
 225 230 235 240  
 Arg Thr Asn Glu Asp Lys Ser Ala Ile Leu Leu Asn Ala Lys Tyr Lys  
 245 250 255  
 Glu Lys Ile Asp Tyr Thr Val Ala Ser Glu Leu Ser Ala Lys Asn Glu  
 260 265 270  
 Lys Phe Ser Gly Phe Leu Lys Ser Val Val Asp Tyr Asp Pro Asn His  
 275 280 285  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (112)...(375)

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 Met Lys  
 1  
  
 gct caa aaa agc ggg gtt tat aat gtg ggt tat tcc caa gcc aga agt 165  
 Ala Gln Lys Ser Gly Val Tyr Asn Val Gly Tyr Ser Gln Ala Arg Ser  
 5 10 15  
  
 tat aat gaa atc gtt agc att tta aaa gag cat tta ggg gat ttt aaa 213  
 Tyr Asn Glu Ile Val Ser Ile Leu Lys Glu His Leu Gly Asp Phe Lys  
 20 25 30  
  
 gtg agt tat atc aaa aac cct tat gct ttc ttc caa aag cac acc caa 261  
 Val Ser Tyr Ile Lys Asn Pro Tyr Ala Phe Phe Gln Lys His Thr Gln  
 35 40 45 50  
  
 gca cac att gag cct gct att ttg gat ttg gat tac acc cct tta tac 309  
 Ala His Ile Glu Pro Ala Ile Leu Asp Leu Asp Tyr Thr Pro Leu Tyr  
 55 60 65  
  
 gat ttg gaa agc ggc att aaa gat tat ttg ccc cat atc cat gcg att 357  
 Asp Leu Glu Ser Gly Ile Lys Asp Tyr Leu Pro His Ile His Ala Ile  
 70 75 80



Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr	Tyr	Thr	Leu	Lys	Asp	Phe	Glu		
			75					80					85				
caa	ctc	acc	caa	tac	ctc	caa	gaa	agc	ttg	ttc	aaa	gaa	tta	ggg	ttt	461	
Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser	Leu	Phe	Lys	Glu	Leu	Gly	Phe		
		90					95					100					
aat	ctg	gat	ggc	atc	tat	ttt	tgc	agg	cac	gcc	cca	gaa	gaa	aat	tgc	509	
Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg	His	Ala	Pro	Glu	Glu	Asn	Cys		
		105				110					115						
gct	tgc	agg	aag	cca	aag	cct	tct	ttg	att	ttg	caa	gct	gct	aaa	gag	557	
Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu	Ile	Leu	Gln	Ala	Ala	Lys	Glu		
120					125					130					135		
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His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe	Met	Ile	Gly	Asp	Lys	Glu	Ser		
			140					145					150				
gac	atg	tta	gcc	ggc	ttg	aac	gct	aaa	gtt	aaa	aat	aac	ctt	ttg	ctc	653	
Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys	Val	Lys	Asn	Asn	Leu	Leu	Leu		
			155				160					165					
att	caa	aac	cct	tta	aaa	act	cct	cat	tct	tgg	ata	caa	tgt	aaa	gat	701	
Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His	Ser	Trp	Ile	Gln	Cys	Lys	Asp		
		170					175					180					
ttt	aaa	gag	atg	ata	gat	cta	atc	aaa	taaggacaag	aatgcgttat						748	
Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys									
		185				190											
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agtaatctag	cctt															822	
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<211>	192																
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Cys	Ile	Arg	Met	Asn	Thr	Asn	Lys	Ala	Leu	Phe	Leu	Asp	Arg	Asp	Gly		
			20					25					30				
Ile	Ile	Asn	Ile	Asp	Lys	Gly	Tyr	Val	Ser	Gln	Lys	Glu	Asp	Phe	Glu		
		35				40						45					
Phe	Gln	Lys	Gly	Ile	Phe	Glu	Leu	Leu	Lys	His	Ala	Lys	Ser	Leu	Gly		
	50					55				60							
Tyr	Lys	Leu	Leu	Leu	Ile	Thr	Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr		
65					70				75					80			
Tyr	Thr	Leu	Lys	Asp	Phe	Glu	Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser		
			85					90						95			
Leu	Phe	Lys	Glu	Leu	Gly	Phe	Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg		
		100					105					110					
His	Ala	Pro	Glu	Glu	Asn	Cys	Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu		
		115				120					125						
Ile	Leu	Gln	Ala	Ala	Lys	Glu	His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe		
	130					135					140						
Met	Ile	Gly	Asp	Lys	Glu	Ser	Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys		

145		150		155		160									
Val	Lys	Asn	Asn	Leu	Leu	Leu	Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His
		165		170		175									
Ser	Trp	Ile	Gln	Cys	Lys	Asp	Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys
		180				185						190			

<210> 73  
 <211> 831  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (88)...(756)

<400> 73

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			Met Pro Ala Arg	Gln Ser Phe Thr	Asp	
			1		5	

ttg	aaa	aac	ctg	gtt	ttg	tgc	gat	ata	ggc	aac	acg	cgt	atc	cat	ttt	162
Leu	Lys	Asn	Leu	Val	Leu	Cys	Asp	Ile	Gly	Asn	Thr	Arg	Ile	His	Phe	
10				15					20						25	

gca	caa	aac	tat	cag	ctc	ttt	tca	agc	gct	aaa	gaa	gat	tta	aag	cgt	210
Ala	Gln	Asn	Tyr	Gln	Leu	Phe	Ser	Ser	Ala	Lys	Glu	Asp	Leu	Lys	Arg	
			30						35					40		

ttg	ggt	att	caa	aag	gaa	att	ttt	tac	att	agc	gtg	aat	gaa	gaa	aat	258
Leu	Gly	Ile	Gln	Lys	Glu	Ile	Phe	Tyr	Ile	Ser	Val	Asn	Glu	Glu	Asn	
			45					50					55			

gaa	aaa	gcc	ctt	ttg	aat	tgt	tac	cct	aac	gct	aaa	aat	att	gca	ggg	306
Glu	Lys	Ala	Leu	Leu	Asn	Cys	Tyr	Pro	Asn	Ala	Lys	Asn	Ile	Ala	Gly	
		60					65						70			

ttt	ttt	cat	tta	gaa	acc	gac	tat	gta	ggg	ctt	ggg	ata	gac	cgg	caa	354
Phe	Phe	His	Leu	Glu	Thr	Asp	Tyr	Val	Gly	Leu	Gly	Ile	Asp	Arg	Gln	
		75				80					85					

atg	gcg	tgt	ctg	gcg	gta	aat	aat	ggc	gtg	gtg	gtg	gat	gcc	ggg	agt	402
Met	Ala	Cys	Leu	Ala	Val	Asn	Asn	Gly	Val	Val	Val	Asp	Ala	Gly	Ser	
90					95				100					105		

gcg	att	acg	ata	gat	tta	atc	aaa	gag	ggc	aag	cat	tta	gga	ggg	tgt	450
Ala	Ile	Thr	Ile	Asp	Leu	Ile	Lys	Glu	Gly	Lys	His	Leu	Gly	Gly	Cys	
				110					115					120		

att	tta	ccc	ggt	tta	gcc	caa	tat	att	cat	gcg	tat	aaa	aaa	agc	gct	498
Ile	Leu	Pro	Gly	Leu	Ala	Gln	Tyr	Ile	His	Ala	Tyr	Lys	Lys	Ser	Ala	
			125					130						135		

aaa	att	tta	gag	caa	cct	ttc	aag	gcc	tta	gat	tct	tta	gaa	gtt	tta	546
Lys	Ile	Leu	Glu	Gln	Pro	Phe	Lys	Ala	Leu	Asp	Ser	Leu	Glu	Val	Leu	
		140					145						150			

cct	aaa	agc	act	aga	gac	gct	gtg	aat	tac	ggc	atg	gtt	ttg	agc	gtc	594
Pro	Lys	Ser	Thr	Arg	Asp	Ala	Val	Asn	Tyr	Gly	Met	Val	Leu	Ser	Val	





Table 1. Mean values of the variables measured in the 1000 m time trial	
Variable	Mean (SD)
Age (years)	22.5 (1.5)
Height (cm)	178.5 (5.5)
Weight (kg)	75.5 (10.5)
VO <sub>2max</sub> (l·min <sup>-1</sup> )	4.5 (0.5)
VO <sub>2max</sub> (ml·kg <sup>-1</sup> ·min <sup>-1</sup> )	59.5 (5.5)
VO <sub>2</sub> at 1000 m (l·min <sup>-1</sup> )	3.5 (0.5)
VO <sub>2</sub> at 1000 m (ml·kg <sup>-1</sup> ·min <sup>-1</sup> )	45.5 (5.5)
Heart rate at 1000 m (b·min <sup>-1</sup> )	165 (10)
Heart rate at 1000 m (b·min <sup>-1</sup> ·kg <sup>-1</sup> )	2.1 (0.1)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> )	46.5 (5.5)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> )	1.1 (0.1)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.6 (0.1)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.2 (0.05)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.1 (0.02)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.05 (0.01)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.02 (0.005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.01 (0.001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.005 (0.001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.001 (0.0005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.0005 (0.0001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.0001 (0.00005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.00005 (0.00001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.00001 (0.000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.000005 (0.000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.000001 (0.0000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000005 (0.0000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000001 (0.00000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000005 (0.00000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000001 (0.000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000005 (0.000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000001 (0.0000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000005 (0.0000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000001 (0.00000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000005 (0.00000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000001 (0.000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000000005 (0.000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000000001 (0.0000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000000005 (0.0000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000000001 (0.00000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000000005 (0.00000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000000001 (0.000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000000000005 (0.000000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000000000001 (0.0000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000000000005 (0.0000000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000000000001 (0.00000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000000000005 (0.00000000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000000000001 (0.000000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000000000000005 (0.000000000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.000000000000000001 (0.0000000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000000000000005 (0.0000000000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.0000000000000000001 (0.00000000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000000000000005 (0.00000000000000000001)
Heart rate at 1000 m (b·min <sup>-1</sup> ·ml <sup>-1</sup> ·kg <sup>-1</sup> )	0.00000000000000000001 (0.000000000000000000005)
Heart rate at 1000 m (b·min <sup>-1</sup> ·l <sup>-</sup>	

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attatgtgat	aatcaccaca	agtaatcggc	ttagtgtcac	attacgaaga	ttaaatgaca	180
taaaaggaaa	aaag atg gtt aat aaa gat gtg aaa	caa acc act gct ttt				230
	Met Val Asn Lys Asp Val Lys	Gln Thr Thr Ala Phe				
	1	5	10			

ggt cct gtt tta tta caa agc act tgg ttt ttg gaa aag tta gcg gcg 326  
Gly Pro Val Leu Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala  
30 35 40

ttt gac aga gaa aga atc cct gaa agg gtg gtg cat gct aaa gga agc 374  
Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser  
45 50 55 60

gga gct tat ggc act ttc act gtg act aaa gac atc act aaa tac act 422  
Gly Ala Tyr Gly Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr  
65 70 75

aaa gcg aaa att ttc tct aaa gtg ggc aaa aaa acc gaa tgc ttc ttc 470  
Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe  
80 85 90

aga ttt tct act gtg gct ggt gaa aga ggc agt gcg gat gcg gtg aga 518  
Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg  
95 100 105

gac cct aga ggt ttt gcg atg aag tat tac act gaa gaa ggt aac tgg 566  
Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp  
110 115 120

gat tta gtg ggg aac aac acg cct gtt ttc ttt atc cgt gat gcg atc 614  
Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile  
125 130 135 140

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Lys Phe Pro Asp Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn  
145 150 155

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 160 165 170

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 Ser Leu Tyr Gln Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys  
 175 180 185

tct ttc cgc cac atg gat ggt ttt ggc agc cac act ttc agt ctt atc 806  
Ser Phe Arg His Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile  
190 195 200







aat gaa gaa gac ttg tta gtg agt aaa aaa cgc ttg gat aaa atc tat 248  
 Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile Tyr  
 55 60 65

cgt tta aaa cag cgc gtt tta ggg act ctt gga gga ata aat cca aac 296  
 Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro Asn  
 70 75 80

ttt aaa aaa gaa att tta gag tgc atg caa gat gat tta aac gtt tct 344  
 Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val Ser  
 85 90 95

aaa gcg ttg agc gtt tta gaa agc atg ctt tct tcc act aat gaa aaa 392  
 Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu Lys  
 100 105 110

ttg gat caa aac cct aaa aac aag gct tta aag ggc gaa att tta gcg 440  
 Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu Ala  
 115 120 125 130

aat ttg aaa ttc ata gaa gaa ctg ctt ggc atc ggg ttt aaa gac cct 488  
 Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp Pro  
 135 140 145

agc gcc tat ttc caa tta ggc gtg agt gaa agc gaa aaa caa gaa att 536  
 Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu Ile  
 150 155 160

gaa aac aag ata gaa gaa aga aaa cgc gcc aaa gag cga aaa gat ttt 584  
 Glu Asn Lys Ile Glu Glu Arg Lys Arg Ala Lys Glu Arg Lys Asp Phe  
 165 170 175

tta aaa gcc gat agc atc aga gaa gag ctt ttg aaa caa aaa atc gct 632  
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 180 185 190

ttg atg gac acc cca caa ggc acg atc tgg gag aag ttt ttt 674  
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 195 200 205

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 <212> PRT  
 <213> Helicobacter pylori

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 Glu Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu  
 35 40 45  
 Asn Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys  
 50 55 60  
 Ile Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn  
 65 70 75 80  
 Pro Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn

Table 1. Demographic characteristics of the study population	
Age (years)	65.8 ± 1.2
Gender (male/female)	10/10
Education (years)	12.5 ± 0.5
Occupation (white/blue)	10/10
Marital status (married/divorced/widowed)	10/10/0
Smoking status (smoker/nonsmoker)	10/10
Alcohol consumption (yes/no)	10/10
Comorbidities (hypertension/diabetes/cholesterol)	10/10/10
Medication (antihypertensive/antidiabetic/anticholesterol)	10/10/10
Family history (hypertension/diabetes/cholesterol)	10/10/10
Physical activity (sedentary/active)	10/10
Stress level (low/moderate/high)	10/10/10
Sleep quality (good/poor)	10/10
Depression score (0-10)	2.5 ± 0.5
Overall health status (good/fair/poor)	10/10/10

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<220>  
<221> CDS  
<222> (60) ... (329)
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<210> 80
<211> 90
<212> PRT
<213> Helicobacter pylori
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20           25           30
Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln Phe Gln Asp His Ala
35           40           45
Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys His Ile Lys Pro Asp
50           55           60
Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu Leu Ile Leu Leu Arg
65           70           75           80
Leu Gly Ser His Ser Glu Leu Phe
85

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 <222> (111)...(779)

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Met Gln
1

ggt tta tgg att tat cca gag gat aca gaa gtt tta ggg gtt gct tgt 164
Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val Ala Cys
5 10 15

aag agc ctt tta aaa gca cta acg cca cgc tat caa aaa gtc gcc ttg 212
Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val Ala Leu
20 25 30

ttt tcg ccc att agt gga ggg tgt gag agc ttg gag gag tgc gag agc 260
Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys Glu Ser
35 40 45 50

ttg aac cct tta gaa ttt cat agt gcg ata agc aaa caa aag gct tta 308
Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys Ala Leu
55 60 65

gag ctt gcg agc acc gct caa gaa gag tta cta ttt gaa acg att ctc 356
Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr Ile Leu
70 75 80

aaa cgc tat gat gaa tta caa tcc acg cat gat ttt gtc att aat ttg 404
Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile Asn Leu
85 90 95

ggg tgt gcg ccg aag ttt ttc tta aac gct cct tta gat tta aac acc 452
Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu Asn Thr
100 105 110

att tta gcc aag cat tta aac gct tct gtt gtg gct gtc gcg caa acg 500
Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala Gln Thr
115 120 125 130

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Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys Lys Glu
              135                      140                      145

gcc cct ttc gct gta ggg tta ttt gcg ggc gaa acg ctt gaa aaa cca      596
Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu Lys Pro
              150                      155                      160

cat ttt tta agc atg tct ctt tgc aag caa caa tgc gaa tta gaa gcg      644
His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu Glu Ala
              165                      170                      175

gat ctg att gaa agc gtg ttg caa ata aaa agc gag att att acc cct      692
Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile Thr Pro
              180                      185                      190

tta gcc ttt caa agg ggt ttg gaa aaa aag gct aaa aaa cag att aaa      740
Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln Ile Lys
              195                      200                      205                      210

aaa gtg gtt tta cca gag agc gaa aag atg aaa gga ttt tgaaagctgc      789
Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe
              215                      220

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 20          25          30
Ala Leu Phe Ser Pro Ile Ser Gly Cys Glu Ser Leu Glu Glu Cys
 35          40          45
Glu Ser Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys
 50          55          60
Ala Leu Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr
 65          70          75          80
Ile Leu Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile
 85          90          95
Asn Leu Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu
100          105          110
Asn Thr Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala
115          120          125
Gln Thr Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys
130          135          140
Lys Glu Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu
145          150          155          160
Lys Pro His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu
165          170          175
Glu Ala Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile
180          185          190
Thr Pro Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln
195          200          205
Ile Lys Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe

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210

215

220

&lt;210&gt; 85

&lt;211&gt; 821

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

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&lt;222&gt; (79)...(753)

&lt;400&gt; 85

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Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln  
 1 5 10

tat ttt gat ttt aga gcc gcc ggt ttt gtc caa ttg att tct aat tac 159  
 Tyr Phe Asp Phe Arg Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr  
 15 20 25

atc aat caa ttt tct tca acg ctt ttt gta acc aac ttg ccc gca caa 207  
 Ile Asn Gln Phe Ser Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln  
 30 35 40

gat att att tat gtg cct ggt tat gaa gtt tca ggg acg gct aaa tac 255  
 Asp Ile Ile Tyr Val Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr  
 45 50 55

aag ggc ttt tct tta ggc ttg agc gtg gcg cga tca tgg cct tct tta 303  
 Lys Gly Phe Ser Leu Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu  
 60 65 70 75

aag ggg cgt ttg atc gct gat gtg tat gaa ttg gcg gcc acg aca ggc 351  
 Lys Gly Arg Leu Ile Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly  
 80 85 90

aat gtg ttt att ttg acg gca agt tat aaa atc cca cgc act ggt ctt 399  
 Asn Val Phe Ile Leu Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu  
 95 100 105

agc atc act tgg ctt tca cgc ttc gtt acg gat ttg agt tat tgc tct 447  
 Ser Ile Thr Trp Leu Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser  
 110 115 120

tat agc cct tat cgt aac ggc cct acg gat att gac aga cgg cct agt 495  
 Tyr Ser Pro Tyr Arg Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser  
 125 130 135

aat tgc cct aaa acg ccc ggg att ttt cat gtt cat aaa ccc ggt tat 543  
 Asn Cys Pro Lys Thr Pro Gly Ile Phe His Val His Lys Pro Gly Tyr  
 140 145 150 155

ggg gtg agc agt ttt ttt gta acc tac aaa ccc acc tat aag aag ctt 591  
 Gly Val Ser Ser Phe Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu  
 160 165 170

aaa ggg ttg agc ttg aat gcg gtg ttt aac aat gtt ttt aac caa caa 639  
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Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser	
1 5 10 15	
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Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu	
20 25 30	
gtg cct ttg tat gaa ttt agt aac acg ggc gaa cat gcc gtt att caa	203
Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln	
35 40 45	
gtg agg aaa agc ggt tta agc act tta gaa atg ctt cag att ttt tct	251
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser	
50 55 60	
caa att tta ggg gta aga atc gct gaa ttg ggt tat gcg ggc ttg aaa	299
Gln Ile Leu Gly Val Arg Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys	
65 70 75 80	
gat aaa aac gcg ctg acg act caa ttc atc tca ctc cct aaa aaa tac	347
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr	
85 90 95	
gcc cct tta tta gaa aaa aat acg agc aac ttt caa gaa aaa aac ctt	395
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu	
100 105 110	
aaa atc ctg tct ttg aat tac cac cac aat aaa atc aaa ttg ggg cat	443
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His	
115 120 125	
ttg aaa ggg aat cgc ttt ttt atg cgt ttt aaa aaa atg acc cct cta	491
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu	
130 135 140	
aac gct caa aaa aca aag cag gtt tta gaa caa atc gcg cag ttt gga	539
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly	
145 150 155 160	
atg cct aat tat ttt ggc tcg caa cgc ttt ggg aag ttc aat gac aac	587
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn	
165 170 175	
cac caa gag ggt tta aaa atc tta caa aat caa acg aaa ttc gcc cat	635
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His	
180 185 190	
caa aaa tta aac gct ttt tta att tca agc tat caa agt tat ttg ttt	683
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe	
195 200 205	
aac gcg ctt tta agc aaa cga tta gaa atc agt aaa atc att agc gct	731
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala	

210						215				220								
ttt	agt	gtc	aaa	gaa	aat	tta	gaa	ttt	ttt	aaa	caa	aaa	aat	tta	agc	779		
Phe	Ser	Val	Lys	Glu	Asn	Leu	Glu	Phe	Phe	Lys	Gln	Lys	Asn	Leu	Ser			
225					230				235					240				
gtt	gat	tca	gac	act	cta	aaa	acc	ctt	aaa	aac	caa	gcc	cac	ccc	ttt	827		
Val	Asp	Ser	Asp	Thr	Leu	Lys	Thr	Leu	Lys	Asn	Gln	Ala	His	Pro	Phe			
245					250				255									
aaa	atc	tta	gaa	ggc	gat	gtg	atg	tgc	cat	tac	cct	tat	ggg	aag	ttt	875		
Lys	Ile	Leu	Glu	Gly	Asp	Val	Met	Cys	His	Tyr	Pro	Tyr	Gly	Lys	Phe			
260					265				270									
ttt	gac	gct	tta	gaa	tta	gaa	aaa	gag	ggc	gaa	agg	ttt	ttg	aaa	aaa	923		
Phe	Asp	Ala	Leu	Glu	Leu	Glu	Lys	Glu	Gly	Glu	Arg	Phe	Leu	Lys	Lys			
275					280				285									
gaa	gtt	gcg	cct	acg	ggg	tta	cta	gac	ggc	aaa	aaa	gct	ctt	tat	gca	971		
Glu	Val	Ala	Pro	Thr	Gly	Leu	Leu	Asp	Gly	Lys	Lys	Ala	Leu	Tyr	Ala			
290					295				300									
aaa	aat	ttg	agt	tta	gaa	att	gaa	aaa	gaa	ttc	cag	cat	aac	ctt	tta	1019		
Lys	Asn	Leu	Ser	Leu	Glu	Ile	Glu	Lys	Glu	Phe	Gln	His	Asn	Leu	Leu			
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agt	agc	cat	gct	aaa	acg	cta	ggc	tct	agg	cgg	ttt	ttt	tgg	gtg	ttt	1067		
Ser	Ser	His	Ala	Lys	Thr	Leu	Gly	Ser	Arg	Arg	Phe	Phe	Trp	Val	Phe			
325					330				335									
gta	gaa	aat	gta	act	tct	caa	tac	gtg	aaa	gaa	aaa	gcg	caa	ttt	gaa	1115		
Val	Glu	Asn	Val	Thr	Ser	Gln	Tyr	Val	Lys	Glu	Lys	Ala	Gln	Phe	Glu			
340					345				350									
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Leu	Gly	Phe	Tyr	Leu	Pro	Lys	Gly	Ser	Tyr	Ala	Ser	Ala	Leu	Leu	Lys			
355					360				365									
gaa	atc	aag	cat	gag	aaa	gga	gaa	aat	aat	gac	gaa	ttt	tgaaaa	agatt	1212			
Glu	Ile	Lys	His	Glu	Lys	Gly	Glu	Asn	Asn	Asp	Glu	Phe						
370					375				380									
atcgcgcgcaaa			acaggatcaa			aacgaacgcg			gttttagcga			cttattgcgt			gattttttgct			1272
tttatcgggt			tgtttgggtgga			tgtcattaga			attaatgcta			atgatttagg			aatagctcct			1332
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<210> 88
<211> 381
<212> PRT
<213> Helicobacter pylori
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<400> 88															
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			20					25					30		
Val	Pro	Leu	Tyr	Glu	Phe	Ser	Asn	Thr	Gly	Glu	His	Ala	Val	Ile	Gln
		35					40					45			
Val	Arg	Lys	Ser	Gly	Leu	Ser	Thr	Leu	Glu	Met	Leu	Gln	Ile	Phe	Ser

50		55		60
Gln Ile Leu Gly Val Arg	Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys			
65	70	75	80	
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr				
	85	90	95	
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu				
	100	105	110	
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His				
	115	120	125	
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu				
	130	135	140	
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly				
	145	150	155	160
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn				
	165	170	175	
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His				
	180	185	190	
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe				
	195	200	205	
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala				
	210	215	220	
Phe Ser Val Lys Glu Asn Leu Glu Phe Phe Lys Gln Lys Asn Leu Ser				
	225	230	235	240
Val Asp Ser Asp Thr Leu Lys Thr Leu Lys Asn Gln Ala His Pro Phe				
	245	250	255	
Lys Ile Leu Glu Gly Asp Val Met Cys His Tyr Pro Tyr Gly Lys Phe				
	260	265	270	
Phe Asp Ala Leu Glu Leu Glu Lys Glu Gly Glu Arg Phe Leu Lys Lys				
	275	280	285	
Glu Val Ala Pro Thr Gly Leu Leu Asp Gly Lys Lys Ala Leu Tyr Ala				
	290	295	300	
Lys Asn Leu Ser Leu Glu Ile Glu Lys Glu Phe Gln His Asn Leu Leu				
	305	310	315	320
Ser Ser His Ala Lys Thr Leu Gly Ser Arg Arg Phe Phe Trp Val Phe				
	325	330	335	
Val Glu Asn Val Thr Ser Gln Tyr Val Lys Glu Lys Ala Gln Phe Glu				
	340	345	350	
Leu Gly Phe Tyr Leu Pro Lys Gly Ser Tyr Ala Ser Ala Leu Leu Lys				
	355	360	365	
Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp Glu Phe				
	370	375	380	

<210> 89  
 <211> 1080  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (76)...(828)

<400> 89

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ccagatccct	taaaa	atg aaa	ctc ccg	gtc gtt	gag agc	111
	Met	Lys	Leu	Pro	Val	
	1		5		10	

caa ggt	gaa gga	aaa agg	ata ggc	aag ccc	agt ctt	ttt ttg	cgc tta	159
Gln Gly	Glu Gly	Lys Arg	Ile Gly	Lys Pro	Ser Leu	Phe Leu	Arg Leu	

15							20				25							
ggg	ggg	tgt	aac	ctt	tca	tgc	aag	ggc	ttt	aat	tgt	aaa	acc	tta	ttg	207		
Gly	Gly	Cys	Asn	Leu	Ser	Cys	Lys	Gly	Phe	Asn	Cys	Lys	Thr	Leu	Leu			
30						35				40								
aat	gat	gaa	atc	cta	aca	ggg	tgc	gac	agc	ttg	tat	gcg	gtg	cat	ccc	255		
Asn	Asp	Glu	Ile	Leu	Thr	Gly	Cys	Asp	Ser	Leu	Tyr	Ala	Val	His	Pro			
45					50				55						60			
aaa	ttc	aaa	aca	tct	tgg	gat	tat	tat	aat	gag	cct	aag	ccc	ttg	att	303		
Lys	Phe	Lys	Thr	Ser	Trp	Asp	Tyr	Tyr	Asn	Glu	Pro	Lys	Pro	Leu	Ile			
				65				70						75				
gaa	cga	tta	gag	gat	tta	gcc	cct	aat	tat	aag	gat	ttt	gat	ttc	att	351		
Glu	Arg	Leu	Glu	Asp	Leu	Ala	Pro	Asn	Tyr	Lys	Asp	Phe	Asp	Phe	Ile			
		80						85				90						
ctt	aca	ggc	ggg	gag	cca	agc	ttg	tat	ttc	aat	aac	cct	att	tta	atc	399		
Leu	Thr	Gly	Gly	Glu	Pro	Ser	Leu	Tyr	Phe	Asn	Asn	Pro	Ile	Leu	Ile			
		95				100						105						
agc	gtt	tta	gag	cat	ttt	tat	cgc	caa	aaa	atc	cct	tta	tgt	gta	gag	447		
Ser	Val	Leu	Glu	His	Phe	Tyr	Arg	Gln	Lys	Ile	Pro	Leu	Cys	Val	Glu			
110						115				120								
agt	aat	ggg	tct	att	ttt	ttt	gaa	ttt	agc	cct	att	tta	aaa	gaa	ttg	495		
Ser	Asn	Gly	Ser	Ile	Phe	Phe	Glu	Phe	Ser	Pro	Ile	Leu	Lys	Glu	Leu			
125					130				135						140			
cat	ttc	act	cta	agc	gtc	aaa	ctc	tct	ttt	tct	tta	gag	gaa	gaa	agc	543		
His	Phe	Thr	Leu	Ser	Val	Lys	Leu	Ser	Phe	Ser	Leu	Glu	Glu	Glu	Ser			
				145				150						155				
aag	cgg	atc	cat	ctt	aaa	gcc	tta	caa	aat	atc	tta	aat	aac	gct	aaa	591		
Lys	Arg	Ile	His	Leu	Lys	Ala	Leu	Gln	Asn	Ile	Leu	Asn	Asn	Ala	Lys			
		160						165				170						
agc	gcg	cat	ttt	aaa	ttt	gtt	tta	gag	agc	caa	aac	gcc	gct	caa	tct	639		
Ser	Ala	His	Phe	Lys	Phe	Val	Leu	Glu	Ser	Gln	Asn	Ala	Ala	Gln	Ser			
		175				180						185						
att	ata	gaa	att	caa	agc	ctc	ttg	aaa	caa	ctc	tcc	tta	aaa	aat	aat	687		
Ile	Ile	Glu	Ile	Gln	Ser	Leu	Leu	Lys	Gln	Leu	Ser	Leu	Lys	Asn	Asn			
190						195				200								
gaa	atc	ttt	tta	atg	cct	tta	ggc	aca	aat	aac	aac	gag	cta	gac	aaa	735		
Glu	Ile	Phe	Leu	Met	Pro	Leu	Gly	Thr	Asn	Asn	Asn	Glu	Leu	Asp	Lys			
205					210				215						220			
aat	cta	aaa	acc	cta	gcc	ccc	cta	gcc	ata	aag	cat	ggg	ttc	agg	cta	783		
Asn	Leu	Lys	Thr	Leu	Ala	Pro	Leu	Ala	Ile	Lys	His	Gly	Phe	Arg	Leu			
				225				230						235				



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atcttatgct gagcgtatcg ctgacaaccc tttagggttt atccaacgct tggatctttt 948
gcctagtatt agcgggttcg ttcaaaaatt ggcgcgagcat ggcggggaat tttttgaaat 1008
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cgagctgtgc aa 1080

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<210> 90
<211> 251
<212> PRT
<213> Helicobacter pylori

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Lys Arg Ile Gly Lys Pro Ser Leu Phe Leu Arg Leu Gly Gly Cys Asn
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Leu Ser Cys Lys Gly Phe Asn Cys Lys Thr Leu Leu Asn Asp Glu Ile
35 40 45
Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val His Pro Lys Phe Lys Thr
50 55 60
Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro Leu Ile Glu Arg Leu Glu
65 70 75 80
Asp Leu Ala Pro Asn Tyr Lys Asp Phe Asp Phe Ile Leu Thr Gly Gly
85 90 95
Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Ile Ser Val Leu Glu
100 105 110
His Phe Tyr Arg Gln Lys Ile Pro Leu Cys Val Glu Ser Asn Gly Ser
115 120 125
Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys Glu Leu His Phe Thr Leu
130 135 140
Ser Val Lys Leu Ser Phe Ser Leu Glu Glu Glu Ser Lys Arg Ile His
145 150 155 160
Leu Lys Ala Leu Gln Asn Ile Leu Asn Asn Ala Lys Ser Ala His Phe
165 170 175
Lys Phe Val Leu Glu Ser Gln Asn Ala Ala Gln Ser Ile Ile Glu Ile
180 185 190
Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys Asn Asn Glu Ile Phe Leu
195 200 205
Met Pro Leu Gly Thr Asn Asn Asn Glu Leu Asp Lys Asn Leu Lys Thr
210 215 220
Leu Ala Pro Leu Ala Ile Lys His Gly Phe Arg Leu Ser Asp Arg Leu
225 230 235 240
His Ile Arg Leu Trp Asp Asn Gln Lys Gly Phe
245 250

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<210> 91
<211> 1710
<212> DNA
<213> Helicobacter pylori

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<220>
<221> CDS
<222> (120)...(1559)

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gattttattc ggtgggattg tcagcatcaa gcctcattgt tcctattagc gttatttta 119
atg gtg gtt ttt act aaa aga gtc gca ctc tcg tta ttt gtg ggc att 167
Met Val Val Phe Thr Lys Arg Val Ala Leu Ser Leu Phe Val Gly Ile
1 5 10 15

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tta gtg agc gct gtt tta atg cat tcg tta cac ctt tcc caa ctc gta Leu Val Ser Ala Val Leu Met His Ser Leu His Leu Ser Gln Leu Val 20 25 30	215
gaa tat att tat cat aaa atc act tcc gtt ttt tac act tac gag cca Glu Tyr Ile Tyr His Lys Ile Thr Ser Val Phe Tyr Thr Tyr Glu Pro 35 40 45	263
gaa aag ggg ctt aat ttc aat ctt tcc aac ctc tat gtt ttt ggg ttt Glu Lys Gly Leu Asn Phe Asn Leu Ser Asn Leu Tyr Val Phe Gly Phe 50 55 60	311
tta atc ttt tta ggc gtc tta agc caa gtg att tta aaa tcc ggt agc Leu Ile Phe Leu Gly Val Leu Ser Gln Val Ile Leu Lys Ser Gly Ser 65 70 75 80	359
gtg caa aac ttt gtc aaa aaa gct aaa aaa tac tca aaa aac gct aaa Val Gln Asn Phe Val Lys Lys Ala Lys Lys Tyr Ser Lys Asn Ala Lys 85 90 95	407
act ccc gaa ttt atc gcc ttt ttt tca ggt atc att att ttt gta gat Thr Pro Glu Phe Ile Ala Phe Phe Ser Gly Ile Ile Ile Phe Val Asp 100 105 110	455
gat tat ttt aac gcc cta acc gtg ggg caa atc tca aag tct tta aac Asp Tyr Phe Asn Ala Leu Thr Val Gly Gln Ile Ser Lys Ser Leu Asn 115 120 125	503
gac gct cat aac tcc aca cga gag cgc ttg gct tat att ata gac tcc Asp Ala His Asn Ser Thr Arg Glu Arg Leu Ala Tyr Ile Ile Asp Ser 130 135 140	551
act tca gcg ccg gtg tgc ttg cta gtc ccc att tct agt tgg ggg gcg Thr Ser Ala Pro Val Cys Leu Leu Val Pro Ile Ser Ser Trp Gly Ala 145 150 155 160	599
tat att atg ggg atc atg aat aac gac agc tcg ccc tta tta aaa gat Tyr Ile Met Gly Ile Met Asn Asn Asp Ser Ser Pro Leu Leu Lys Asp 165 170 175	647
agt ttt tcg gtg ctt gtg caa agc tta agc agt aat tat tat gcg att Ser Phe Ser Val Leu Val Gln Ser Leu Ser Ser Asn Tyr Tyr Ala Ile 180 185 190	695
ttt gca ctc att gca gtc ttt ctc acc att tta tgg caa atc aac ctc Phe Ala Leu Ile Ala Val Phe Leu Thr Ile Leu Trp Gln Ile Asn Leu 195 200 205	743
cct agc atg aga aag tat caa aac ata ggc gtg aag gat ttt tat agc Pro Ser Met Arg Lys Tyr Gln Asn Ile Gly Val Lys Asp Phe Tyr Ser 210 215 220	791
gaa caa gaa gaa agc tct tca aaa cta gcc ccc ttg agt ttg tta ccc Glu Gln Glu Glu Ser Ser Ser Lys Leu Ala Pro Leu Ser Leu Leu Pro 225 230 235 240	839
ctt tct att tta ttg ttg att gtg tcc att tca tca ttg ctt ttt tat Leu Ser Ile Leu Leu Leu Ile Val Ser Ile Ser Ser Leu Leu Phe Tyr	887

	245	250	255	
aca gga gtg att tta aaa aac act gat gcg agt ttt tcg ctc ttt tat	Thr Gly Val Ile Leu Lys Asn Thr Asp Ala Ser Phe Ser Leu Phe Tyr	935		
	260	265	270	
gga ggg ttg ttt tcg ctc atc gtt act tat ctt tta gct tat aag ttt	Gly Gly Leu Phe Ser Leu Ile Val Thr Tyr Leu Leu Ala Tyr Lys Phe	983		
	275	280	285	
tta gaa aaa ggg agc ttt ttt aaa ctc atg ttg gat ggc ttt aag agt	Leu Glu Lys Gly Ser Phe Phe Lys Leu Met Leu Asp Gly Phe Lys Ser	1031		
	290	295	300	
gtg ggg ccg gcg ata cta gtc tta acg ctc gct tgg gct atc ggg cct	Val Gly Pro Ala Ile Leu Val Leu Thr Leu Ala Trp Ala Ile Gly Pro	1079		
	305	310	315	320
gtg att aga gat gac gct caa aca ggg ctt tac ttg gct aac atc agc	Val Ile Arg Asp Asp Ala Gln Thr Gly Leu Tyr Leu Ala Asn Ile Ser	1127		
	325	330	335	
aag ggg ttt tta aat aat gga gga ggc gtg tat atg cct tta atc ttt	Lys Gly Phe Leu Asn Asn Gly Gly Gly Val Tyr Met Pro Leu Ile Phe	1175		
	340	345	350	
ttt tta atc tct ggg ttt atc gct ttt tct acc ggc aca agc tgg gga	Phe Leu Ile Ser Gly Phe Ile Ala Phe Ser Thr Gly Thr Ser Trp Gly	1223		
	355	360	365	
gcg ttt gcg atc atg ctt ccc att gga gcg ggc atg gct agt gaa agc	Ala Phe Ala Ile Met Leu Pro Ile Gly Ala Gly Met Ala Ser Glu Ser	1271		
	370	375	380	
gat att att ttg att gtt tca gcg att ctc tca ggc gcg gtt tat ggc	Asp Ile Ile Leu Ile Val Ser Ala Ile Leu Ser Gly Ala Val Tyr Gly	1319		
	385	390	395	400
gat cac aca agc cct att tct gac acg act ata cta tcg gct acg ggg	Asp His Thr Ser Pro Ile Ser Asp Thr Thr Ile Leu Ser Ala Thr Gly	1367		
	405	410	415	
gca ggg tgt tcg gtg caa agc cat ttt atc acg caa ctc cct tat gcg	Ala Gly Cys Ser Val Gln Ser His Phe Ile Thr Gln Leu Pro Tyr Ala	1415		
	420	425	430	
acc att gcg atg ctt tgc agc gcg gtg agt ttg ggg gtg gca agc ttt	Thr Ile Ala Met Leu Cys Ser Ala Val Ser Leu Gly Val Ala Ser Phe	1463		
	435	440	445	
atg tat tcg cgt tcg ctc gct ctt tta atc ggt gtg gct ttg ctt gtg	Met Tyr Ser Arg Ser Leu Ala Leu Leu Ile Gly Val Ala Leu Leu Val	1511		
	450	455	460	
ggg gtg ttt tat ctt tta aaa aaa ttt tat ggt gaa aat cta aaa act	Gly Val Phe Tyr Leu Leu Lys Lys Phe Tyr Gly Glu Asn Leu Lys Thr	1559		
	465	470	475	480
tgaatattga ttgaagaagc ttaaaaatcc catttttttaa aattaaaata aggtttttatc		1619		

gatccctatt tgactcaaaa agagtcttat tccattatca atcaattaa aaaggttatt  
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1679  
 1710

<210> 92  
 <211> 480  
 <212> PRT  
 <213> Helicobacter pylori

<400> 92

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			20					25					30		
Glu	Tyr	Ile	Tyr	His	Lys	Ile	Thr	Ser	Val	Phe	Tyr	Thr	Tyr	Glu	Pro
		35					40					45			
Glu	Lys	Gly	Leu	Asn	Phe	Asn	Leu	Ser	Asn	Leu	Tyr	Val	Phe	Gly	Phe
	50					55					60				
Leu	Ile	Phe	Leu	Gly	Val	Leu	Ser	Gln	Val	Ile	Leu	Lys	Ser	Gly	Ser
65					70					75					80
Val	Gln	Asn	Phe	Val	Lys	Lys	Ala	Lys	Lys	Tyr	Ser	Lys	Asn	Ala	Lys
				85					90					95	
Thr	Pro	Glu	Phe	Ile	Ala	Phe	Phe	Ser	Gly	Ile	Ile	Ile	Phe	Val	Asp
			100					105					110		
Asp	Tyr	Phe	Asn	Ala	Leu	Thr	Val	Gly	Gln	Ile	Ser	Lys	Ser	Leu	Asn
		115					120					125			
Asp	Ala	His	Asn	Ser	Thr	Arg	Glu	Arg	Leu	Ala	Tyr	Ile	Ile	Asp	Ser
	130					135					140				
Thr	Ser	Ala	Pro	Val	Cys	Leu	Leu	Val	Pro	Ile	Ser	Ser	Trp	Gly	Ala
145					150					155					160
Tyr	Ile	Met	Gly	Ile	Met	Asn	Asn	Asp	Ser	Ser	Pro	Leu	Leu	Lys	Asp
				165					170					175	
Ser	Phe	Ser	Val	Leu	Val	Gln	Ser	Leu	Ser	Ser	Asn	Tyr	Tyr	Ala	Ile
			180					185					190		
Phe	Ala	Leu	Ile	Ala	Val	Phe	Leu	Thr	Ile	Leu	Trp	Gln	Ile	Asn	Leu
		195					200					205			
Pro	Ser	Met	Arg	Lys	Tyr	Gln	Asn	Ile	Gly	Val	Lys	Asp	Phe	Tyr	Ser
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Glu	Gln	Glu	Glu	Ser	Ser	Ser	Lys	Leu	Ala	Pro	Leu	Ser	Leu	Leu	Pro
225					230					235					240
Leu	Ser	Ile	Leu	Leu	Ile	Val	Ser	Ile	Ser	Ser	Leu	Leu	Phe	Tyr	
				245				250					255		
Thr	Gly	Val	Ile	Leu	Lys	Asn	Thr	Asp	Ala	Ser	Phe	Ser	Leu	Phe	Tyr
			260					265					270		
Gly	Gly	Leu	Phe	Ser	Leu	Ile	Val	Thr	Tyr	Leu	Leu	Ala	Tyr	Lys	Phe
		275				280						285			
Leu	Glu	Lys	Gly	Ser	Phe	Phe	Lys	Leu	Met	Leu	Asp	Gly	Phe	Lys	Ser
	290				295						300				
Val	Gly	Pro	Ala	Ile	Leu	Val	Leu	Thr	Leu	Ala	Trp	Ala	Ile	Gly	Pro
305					310					315					320
Val	Ile	Arg	Asp	Asp	Ala	Gln	Thr	Gly	Leu	Tyr	Leu	Ala	Asn	Ile	Ser
			325						330					335	
Lys	Gly	Phe	Leu	Asn	Asn	Gly	Gly	Gly	Val	Tyr	Met	Pro	Leu	Ile	Phe
			340					345					350		
Phe	Leu	Ile	Ser	Gly	Phe	Ile	Ala	Phe	Ser	Thr	Gly	Thr	Ser	Trp	Gly
		355				360						365			
Ala	Phe	Ala	Ile	Met	Leu	Pro	Ile	Gly	Ala	Gly	Met	Ala	Ser	Glu	Ser
	370					375					380				
Asp	Ile	Ile	Leu	Ile	Val	Ser	Ala	Ile	Leu	Ser	Gly	Ala	Val	Tyr	Gly
385					390					395					400

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Asp His Thr Ser Pro Ile Ser Asp Thr Thr Ile Leu Ser Ala Thr Gly
                405                410                415
Ala Gly Cys Ser Val Gln Ser His Phe Ile Thr Gln Leu Pro Tyr Ala
                420                425                430
Thr Ile Ala Met Leu Cys Ser Ala Val Ser Leu Gly Val Ala Ser Phe
                435                440                445
Met Tyr Ser Arg Ser Leu Ala Leu Leu Ile Gly Val Ala Leu Leu Val
                450                455                460
Gly Val Phe Tyr Leu Leu Lys Lys Phe Tyr Gly Glu Asn Leu Lys Thr
465                470                475                480

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<210> 93  
 <211> 629  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (82)...(525)

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<400> 93
caaatctcta aagagtaacg ctttttaaaaa aaatacatatt tttttaatttt tttaaatcaat      60
cattaagggtg ttttaagtta a att tcc tta tct gtt aaa cat acg gat aat      111
                Ile Ser Leu Ser Val Lys His Thr Asp Asn
                1                5                10

ggt ata tct tta agg aaa gaa aat ggg gtt agg aca cta ata agt tta      159
Val Ile Ser Leu Arg Lys Glu Asn Gly Val Arg Thr Leu Ile Ser Leu
                15                20                25

ggg att ttg tta agc gtt ttg agt ggc gat gat ctg aag ttg tat tca      207
Gly Ile Leu Leu Ser Val Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser
                30                35                40

aaa ctt tca gtc tat tcg gct gga agt ggg atg att ggg att gat att      255
Lys Leu Ser Val Tyr Ser Ala Gly Ser Gly Met Ile Gly Ile Asp Ile
                45                50                55

gac aaa cgg aca ttt tat aag cga gcg ttc gct ttc acg atg aaa tcg      303
Asp Lys Arg Thr Phe Tyr Lys Arg Ala Phe Ala Phe Thr Met Lys Ser
                60                65                70

ttg ttc ggt gaa aac ttg ctt ttg ttt gtc aaa tta aag cat tct gcg      351
Leu Phe Gly Glu Asn Leu Leu Leu Phe Val Lys Leu Lys His Ser Ala
                75                80                85                90

ttg acg agc aaa cac atg aaa ggg cct tta gaa aac cgc cat cac cat      399
Leu Thr Ser Lys His Met Lys Gly Pro Leu Glu Asn Arg His His His
                95                100                105

tct ttc act aaa aat tat gaa aaa gcg gtt aat ggt tgt caa aag tat      447
Ser Phe Thr Lys Asn Tyr Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr
                110                115                120

ttc cat att aaa ttg cct gaa ggc gct cct agc aac ttc aaa tca ggt      495
Phe His Ile Lys Leu Pro Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly
                125                130                135

tca tac atg gcc act atg gtg gtg cgt ttt taaagcgtta tttgggggtat      545

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Ser Tyr Met Ala Thr Met Val Val Arg Phe  
140 145

tctttaatac ccttatcgtc ttttaaaata ccatctttta aaagcacaaa tttatttttt 605  
agcccttttt taaatcttct taaa 629

<210> 94  
<211> 148  
<212> PRT  
<213> Helicobacter pylori

<400> 94  
Ile Ser Leu Ser Val Lys His Thr Asp Asn Val Ile Ser Leu Arg Lys  
1 5 10 15  
Glu Asn Gly Val Arg Thr Leu Ile Ser Leu Gly Ile Leu Leu Ser Val  
20 25 30  
Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser Lys Leu Ser Val Tyr Ser  
35 40 45  
Ala Gly Ser Gly Met Ile Gly Ile Asp Ile Asp Lys Arg Thr Phe Tyr  
50 55 60  
Lys Arg Ala Phe Ala Phe Thr Met Lys Ser Leu Phe Gly Glu Asn Leu  
65 70 75 80  
Leu Leu Phe Val Lys Leu Lys His Ser Ala Leu Thr Ser Lys His Met  
85 90 95  
Lys Gly Pro Leu Glu Asn Arg His His His Ser Phe Thr Lys Asn Tyr  
100 105 110  
Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr Phe His Ile Lys Leu Pro  
115 120 125  
Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly Ser Tyr Met Ala Thr Met  
130 135 140  
Val Val Arg Phe  
145

<210> 95  
<211> 626  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (98)...(547)

<400> 95  
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cataagactt caaagatttt ttaaagtttt aacattg atg cgt tgc gtg gtg tat 115  
Met Arg Cys Val Val Tyr  
1 5  
tct atc gct aaa agt tcg cct tta gag tta gtg aaa atc tat caa aag 163  
Ser Ile Ala Lys Ser Ser Pro Leu Glu Leu Val Lys Ile Tyr Gln Lys  
10 15 20  
caa tgc agg caa ttt gat tgc gag ctg gaa ttg gtg gat tta ttc cct 211  
Gln Cys Arg Gln Phe Asp Cys Glu Leu Glu Leu Val Asp Leu Phe Pro  
25 30 35  
aaa aat acc gcc aac gct caa aaa gtt tct aaa aaa ctg gct caa aaa 259  
Lys Asn Thr Ala Asn Ala Gln Lys Val Ser Lys Lys Leu Ala Gln Lys  
40 45 50

agc tac tct cta gct ttt gag ccg tat tta aac cct aag gca aaa aat	307
Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu Asn Pro Lys Ala Lys Asn	
55 60 65 70	
atc gcc tta cac cct aaa gct caa agg ggc gat agc ttt gcg ttt agt	355
Ile Ala Leu His Pro Lys Ala Gln Arg Gly Asp Ser Phe Ala Phe Ser	
75 80 85	
aaa atg tta gaa aat cat ctt aat att aat ttt ttt atc gct gga gcg	403
Lys Met Leu Glu Asn His Leu Asn Ile Asn Phe Phe Ile Ala Gly Ala	
90 95 100	
tat ggg ttt gaa gaa aat ttt tta aag gat tgt caa gct tgg agt ttg	451
Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp Cys Gln Ala Trp Ser Leu	
105 110 115	
agc gag atg act ttt agc cat gaa gtg gct aaa att gtc tta tgc gag	499
Ser Glu Met Thr Phe Ser His Glu Val Ala Lys Ile Val Leu Cys Glu	
120 125 130	
caa atc tat agg gct tta agc att att ttt aag cat cca tac cat aaa	547
Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe Lys His Pro Tyr His Lys	
135 140 145 150	
taggaggtgc gcatgcgttt ttacattatc tttacatttt tgtttattgt ggggttttgg	607
tggtttgttt atagtattg	626

<210> 96  
 <211> 150  
 <212> PRT  
 <213> Helicobacter pylori

<400> 96	
Met Arg Cys Val Val Tyr Ser Ile Ala Lys Ser Ser Pro Leu Glu Leu	
1 5 10 15	
Val Lys Ile Tyr Gln Lys Gln Cys Arg Gln Phe Asp Cys Glu Leu Glu	
20 25 30	
Leu Val Asp Leu Phe Pro Lys Asn Thr Ala Asn Ala Gln Lys Val Ser	
35 40 45	
Lys Lys Leu Ala Gln Lys Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu	
50 55 60	
Asn Pro Lys Ala Lys Asn Ile Ala Leu His Pro Lys Ala Gln Arg Gly	
65 70 75 80	
Asp Ser Phe Ala Phe Ser Lys Met Leu Glu Asn His Leu Asn Ile Asn	
85 90 95	
Phe Phe Ile Ala Gly Ala Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp	
100 105 110	
Cys Gln Ala Trp Ser Leu Ser Glu Met Thr Phe Ser His Glu Val Ala	
115 120 125	
Lys Ile Val Leu Cys Glu Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe	
130 135 140	
Lys His Pro Tyr His Lys	
145 150	

<210> 97  
 <211> 1053  
 <212> DNA  
 <213> Helicobacter pylori







210		215		220
Pro Gly Ala Met Ile Gly Phe Ala Gly Pro Arg Val Ile Lys Gln Thr				
225		230		235
Ile Gly Ala Asp Leu Pro Glu Gly Phe Gln Thr Ala Glu Phe Leu Leu				240
	245		250	255
Glu His Gly Leu Ile Asp Met Ile Val His Arg Lys Asp Leu Lys Lys				
	260		265	270
Thr Leu Ser Asp Leu Ile Ala Met Met Thr His Lys Thr Ser Lys Ile				
	275		280	285
Phe				

<210> 99  
 <211> 810  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (95)...(706)

<400> 99	
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gcttataata aacaaaatta gcttaagagt agtg atg caa ggg ttt ctt tta caa	115
Met Gln Gly Phe Leu Leu Gln	
1 5	
aca caa agc ata aga gat gaa gat ttg atc gtg cgc gtt tta acc aaa	163
Thr Gln Ser Ile Arg Asp Glu Asp Leu Ile Val Arg Val Leu Thr Lys	
10 15 20	
aac cag ctc aaa acc ctc tat cgt ttc tat ggc aaa cgc cat agc gtg	211
Asn Gln Leu Lys Thr Leu Tyr Arg Phe Tyr Gly Lys Arg His Ser Val	
25 30 35	
ctg aat gtg ggg cgt aaa att gat ttt gaa gaa gaa aac gat gat aag	259
Leu Asn Val Gly Arg Lys Ile Asp Phe Glu Glu Glu Asn Asp Asp Lys	
40 45 50 55	
ttt tta ccc aag tta agg aat att ttg cat tta ggc tat att tgg gaa	307
Phe Leu Pro Lys Leu Arg Asn Ile Leu His Leu Gly Tyr Ile Trp Glu	
60 65 70	
aga gaa atg gag cgc ttg ttt ttt tgg caa cgc ttt tgc gct ctc ttg	355
Arg Glu Met Glu Arg Leu Phe Phe Trp Gln Arg Phe Cys Ala Leu Leu	
75 80 85	
ttt agg cat tta gaa ggc gtg cat tct tta gat agc gtc tat ttt gac	403
Phe Arg His Leu Glu Gly Val His Ser Leu Asp Ser Val Tyr Phe Asp	
90 95 100	
act tta gat gat ggg gct aac aaa ctc gcc aaa cag cac ccc tta aga	451
Thr Leu Asp Asp Gly Ala Asn Lys Leu Ala Lys Gln His Pro Leu Arg	
105 110 115	
gtg att tta gaa atg tat gca acg ctt ttg aat ttt gaa ggg cgc ttg	499
Val Ile Leu Glu Met Tyr Ala Thr Leu Leu Asn Phe Glu Gly Arg Leu	
120 125 130 135	



<213> Helicobacter pylori

<220>

<221> CDS

<222> (76)...(927)

<400> 101

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Met Asn Ala Trp Asn Thr Ile Tyr Asp Gln Phe Asn	
1 5 10	
cct atc gct ttt agt ctt ggc agt att gaa gtg cat tgg tat ggt ttg	159
Pro Ile Ala Phe Ser Leu Gly Ser Ile Glu Val His Trp Tyr Gly Leu	
15 20 25	
gcg tat gcg tgt gcg att gtt acc gct ttt tat atg gcg tta aga atg	207
Ala Tyr Ala Cys Ala Ile Val Thr Ala Phe Tyr Met Ala Leu Arg Met	
30 35 40	
atc caa aaa gac ccc aag cga ttc ccc att gaa agg aag gaa ttt gag	255
Ile Gln Lys Asp Pro Lys Arg Phe Pro Ile Glu Arg Lys Glu Phe Glu	
45 50 55 60	
agt tat ttt tta tgg gcg gag ctt ggc att gtg cta ggg gca agg ata	303
Ser Tyr Phe Leu Trp Ala Glu Leu Gly Ile Val Leu Gly Ala Arg Ile	
65 70 75	
gga tac att ctt att tat gag cct aat tct ggc tat tat ttg acg cat	351
Gly Tyr Ile Leu Ile Tyr Glu Pro Asn Ser Gly Tyr Tyr Leu Thr His	
80 85 90	
ttt tgg caa atc ttt aac cct ttt gat agc cat ggg aat ttt gta ggc	399
Phe Trp Gln Ile Phe Asn Pro Phe Asp Ser His Gly Asn Phe Val Gly	
95 100 105	
att cgt ggg atg agc tat cat ggg ggg ttg gtg ggg ttt ttg atc gct	447
Ile Arg Gly Met Ser Tyr His Gly Gly Leu Val Gly Phe Leu Ile Ala	
110 115 120	
tcg tat ctt tat agc cgt aag gat ttg aaa aag ctt ttg att tat ttg	495
Ser Tyr Leu Tyr Ser Arg Lys Asp Leu Lys Lys Leu Leu Ile Tyr Leu	
125 130 135 140	
gat ttg att gcg atc agc ctg cct tta ggg tat gtt ttt ggg agg att	543
Asp Leu Ile Ala Ile Ser Leu Pro Leu Gly Tyr Val Phe Gly Arg Ile	
145 150 155	
ggg aat ttt tta aac cag gag ctt gtg gga aga att gtc ccc aaa gac	591
Gly Asn Phe Leu Asn Gln Glu Leu Val Gly Arg Ile Val Pro Lys Asp	
160 165 170	
agc cat tta ggg caa atc ata ggc att atg gtg gat aat gag ttg cgt	639
Ser His Leu Gly Gln Ile Ile Gly Ile Met Val Asp Asn Glu Leu Arg	
175 180 185	
tat ccc agc caa ttg att gaa gcg ttt tta gag ggg gtt atc gtg ttt	687
Tyr Pro Ser Gln Leu Ile Glu Ala Phe Leu Glu Gly Val Ile Val Phe	
190 195 200	











aaa att tct tta agc ctt caa aac gat gaa tta aaa aac aac ccc gct	350
Lys Ile Ser Leu Ser Leu Gln Asn Asp Glu Leu Lys Asn Asn Pro Ala	
80 85 90 95	
ttt tta aac acg atc caa aaa agc cct gtg gtg cat ctt atg ggt tta	398
Phe Leu Asn Thr Ile Gln Lys Ser Pro Val Val His Leu Met Gly Leu	
100 105 110	
atg agc gat gga ggc gtg cat tca cac att gag cat ttt atc gct ctg	446
Met Ser Asp Gly Gly Val His Ser His Ile Glu His Phe Ile Ala Leu	
115 120 125	
gct tta gag tgt gaa aaa tcc cat aaa aaa gtc tgt ctg cat tta atc	494
Ala Leu Glu Cys Glu Lys Ser His Lys Lys Val Cys Leu His Leu Ile	
130 135 140	
acc gat ggg cgc gat gtc gct cct aaa agc gct tta act tat tta aaa	542
Thr Asp Gly Arg Asp Val Ala Pro Lys Ser Ala Leu Thr Tyr Leu Lys	
145 150 155	
caa atg caa aat atc tgc aat gaa agc att caa atc gct acc ata agc	590
Gln Met Gln Asn Ile Cys Asn Glu Ser Ile Gln Ile Ala Thr Ile Ser	
160 165 170 175	
ggg cgt ttt tat gcc atg gat agg gat aag cgc ttt gaa agg att gag	638
Gly Arg Phe Tyr Ala Met Asp Arg Asp Lys Arg Phe Glu Arg Ile Glu	
180 185 190	
ctt gcg tat cat agc tta atg ggg ctt aat cac acg cct tta agc cct	686
Leu Ala Tyr His Ser Leu Met Gly Leu Asn His Thr Pro Leu Ser Pro	
195 200 205	
agc gag tat atc caa agc cag tat gat aaa aat atc acc gat gaa ttt	734
Ser Glu Tyr Ile Gln Ser Gln Tyr Asp Lys Asn Ile Thr Asp Glu Phe	
210 215 220	
atc atg ccc gct tgt ttt aaa aat tat tgc ggc atg caa gat gat gag	782
Ile Met Pro Ala Cys Phe Lys Asn Tyr Cys Gly Met Gln Asp Asp Glu	
225 230 235	
agt ttt att ttt atc aat ttc agg aat gat agg gct aga gaa atc gtg	830
Ser Phe Ile Phe Ile Asn Phe Arg Asn Asp Arg Ala Arg Glu Ile Val	
240 245 250 255	
agc gct tta ggc caa aaa caa ttc agt ggc ttt aag cgc caa gtt ttt	878
Ser Ala Leu Gly Gln Lys Gln Phe Ser Gly Phe Lys Arg Gln Val Phe	
260 265 270	
aaa aaa ctc cat atc gct acc atg acg cct tat gat aac act ttc ccc	926
Lys Lys Leu His Ile Ala Thr Met Thr Pro Tyr Asp Asn Thr Phe Pro	
275 280 285	
tac cct gtt tta ttc ccc aaa gaa agc gtt caa aac acg ctc gct gaa	974
Tyr Pro Val Leu Phe Pro Lys Glu Ser Val Gln Asn Thr Leu Ala Glu	
290 295 300	
gtg gtc tct caa cac aac ctg acc caa agc cat atc gct gaa act gaa	1022
Val Val Ser Gln His Asn Leu Thr Gln Ser His Ile Ala Glu Thr Glu	

[illegible]

Asp	Leu	Met	Phe	Lys	Thr	Leu	Pro	Tyr	Ser	Leu	Ile	Asp	Thr	His	Gly
		35					40					45			
Leu	Ser	Val	Gly	Leu	Pro	Lys	Gly	Gln	Met	Gly	Asn	Ser	Glu	Val	Gly
	50					55					60				
His	Met	Cys	Ile	Gly	Ala	Gly	Arg	Val	Leu	Tyr	Gln	Asp	Leu	Val	Lys
65					70					75					80
Ile	Ser	Leu	Ser	Leu	Gln	Asn	Asp	Glu	Leu	Lys	Asn	Asn	Pro	Ala	Phe
				85				90						95	
Leu	Asn	Thr	Ile	Gln	Lys	Ser	Pro	Val	Val	His	Leu	Met	Gly	Leu	Met
			100					105					110		
Ser	Asp	Gly	Gly	Val	His	Ser	His	Ile	Glu	His	Phe	Ile	Ala	Leu	Ala
		115					120					125			
Leu	Glu	Cys	Glu	Lys	Ser	His	Lys	Lys	Val	Cys	Leu	His	Leu	Ile	Thr
	130					135					140				
Asp	Gly	Arg	Asp	Val	Ala	Pro	Lys	Ser	Ala	Leu	Thr	Tyr	Leu	Lys	Gln
145					150					155					160
Met	Gln	Asn	Ile	Cys	Asn	Glu	Ser	Ile	Gln	Ile	Ala	Thr	Ile	Ser	Gly
				165					170					175	
Arg	Phe	Tyr	Ala	Met	Asp	Arg	Asp	Lys	Arg	Phe	Glu	Arg	Ile	Glu	Leu
			180					185						190	
Ala	Tyr	His	Ser	Leu	Met	Gly	Leu	Asn	His	Thr	Pro	Leu	Ser	Pro	Ser
		195					200					205			
Glu	Tyr	Ile	Gln	Ser	Gln	Tyr	Asp	Lys	Asn	Ile	Thr	Asp	Glu	Phe	Ile
	210					215					220				
Met	Pro	Ala	Cys	Phe	Lys	Asn	Tyr	Cys	Gly	Met	Gln	Asp	Asp	Glu	Ser
225					230					235					240
Phe	Ile	Phe	Ile	Asn	Phe	Arg	Asn	Asp	Arg	Ala	Arg	Glu	Ile	Val	Ser
				245					250					255	
Ala	Leu	Gly	Gln	Lys	Gln	Phe	Ser	Gly	Phe	Lys	Arg	Gln	Val	Phe	Lys
			260					265					270		
Lys	Leu	His	Ile	Ala	Thr	Met	Thr	Pro	Tyr	Asp	Asn	Thr	Phe	Pro	Tyr
		275					280					285			
Pro	Val	Leu	Phe	Pro	Lys	Glu	Ser	Val	Gln	Asn	Thr	Leu	Ala	Glu	Val
	290					295					300				
Val	Ser	Gln	His	Asn	Leu	Thr	Gln	Ser	His	Ile	Ala	Glu	Thr	Glu	Lys
305					310					315					320
Tyr	Ala	His	Val	Thr	Phe	Phe	Ile	Asn	Gly	Gly	Val	Glu	Thr	Pro	Phe
				325					330					335	
Lys	Asn	Glu	Asn	Arg	Val	Leu	Ile	Gln	Ser	Pro	Lys	Val	Thr	Thr	Tyr
			340					345					350		
Asp	Leu	Lys	Pro	Glu	Met	Ser	Ala	Lys	Glu	Val	Thr	Leu	Ala	Val	Leu
		355					360					365			
Glu	Gln	Met	Lys	Leu	Gly	Thr	Asp	Leu	Ile	Ile	Val	Asn	Phe	Ala	Asn
	370					375					380				
Gly	Asp	Met	Val	Gly	His	Thr	Gly	Asn	Phe	Glu	Ala	Ser	Val	Lys	Ala
385					390					395					400
Val	Glu	Ala	Val	Asp	Ala	Cys	Leu	Gly	Glu	Ile	Leu	Ser	Leu	Ala	Lys
				405					410					415	
Lys	Leu	Asp	Tyr	Ala	Met	Leu	Leu	Thr	Ser	Asp	His	Gly	Asn	Cys	Glu
			420					425					430		
Arg	Met	Lys	Asp	Glu	Asn	Gln	Asn	Pro	Leu	Thr	Asn	His	Thr	Ala	Gly
			435				440						445		
Ser	Val	Tyr	Cys	Phe	Val	Leu	Gly	Asp	Gly	Val	Lys	Ser	Ile	Lys	Asn
	450					455					460				
Gly	Ala	Leu	Asn	Asn	Ile	Ala	Ser	Ser	Val	Leu	Lys	Leu	Met	Gly	Leu
465					470					475					480
Lys	Ala	Pro	Ala	Thr	Met	Asp	Glu	Pro	Leu	Phe					
				485					490						

<210> 107  
 <211> 1440  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (72)...(1379)

<400> 107

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gagtttttaa c atg aat ttt caa gaa aat tta gcc gct ttg gat ttg gag	110
Met Asn Phe Gln Glu Asn Leu Ala Ala Leu Asp Leu Glu	
1 5 10	
tat ctt tgg cac cct tgt tcg caa atg caa gag cat caa aat ttc ccc	158
Tyr Leu Trp His Pro Cys Ser Gln Met Gln Glu His Gln Asn Phe Pro	
15 20 25	
att atc ccc att aaa aag gct caa ggg att tac ctc tat gat ttt aat	206
Ile Ile Pro Ile Lys Lys Ala Gln Gly Ile Tyr Leu Tyr Asp Phe Asn	
30 35 40 45	
gat aac gct tac atg gat ttg atc agc tca tgg tgg gtg aat ctt ttt	254
Asp Asn Ala Tyr Met Asp Leu Ile Ser Ser Trp Trp Val Asn Leu Phe	
50 55 60	
ggg cat aat aac gcc tac atc agc cag caa ctc aaa aat caa att gat	302
Gly His Asn Asn Ala Tyr Ile Ser Gln Gln Leu Lys Asn Gln Ile Asp	
65 70 75	
gat tta gag cat gtc ctt ttg gct tct ttt agc cat aag ccc att atc	350
Asp Leu Glu His Val Leu Leu Ala Ser Phe Ser His Lys Pro Ile Ile	
80 85 90	
acg ctc tct caa agg ctt tgc cag ctc act cat atg gat aaa tgc ttt	398
Thr Leu Ser Gln Arg Leu Cys Gln Leu Thr His Met Asp Lys Cys Phe	
95 100 105	
tat gcg gat aac ggc tca tct tgt gtt gaa atc gct ttg aaa atg agc	446
Tyr Ala Asp Asn Gly Ser Ser Cys Val Glu Ile Ala Leu Lys Met Ser	
110 115 120 125	
tat cac gcc cat ttt tta aag aat caa acg cgc cgc aaa aag ctt ttt	494
Tyr His Ala His Phe Leu Lys Asn Gln Thr Arg Arg Lys Lys Leu Phe	
130 135 140	
tta tcg ctc tct aat tcc tat cat ggc gag act ttg gga gcg tta agc	542
Leu Ser Leu Ser Asn Ser Tyr His Gly Glu Thr Leu Gly Ala Leu Ser	
145 150 155	
gtg ggc gat gtg aaa ctt tat aaa gac act tac acc cct tta ttg ctc	590
Val Gly Asp Val Lys Leu Tyr Lys Asp Thr Tyr Thr Pro Leu Leu Leu	
160 165 170	
aaa aat ctc acc aca cct gtg cct aaa aac gac cat gaa ata gaa aat	638
Lys Asn Leu Thr Thr Pro Val Pro Lys Asn Asp His Glu Ile Glu Asn	
175 180 185	

agt ttg aac gct tta aag cgt ttg tta gac aag cat agt gaa gaa att Ser Leu Asn Ala Leu Lys Arg Leu Leu Asp Lys His Ser Glu Glu Ile 190 195 200 205	686
tgc gct ttc att gca gag cct ctt ttg caa tgc gca ggg aat atg cat Cys Ala Phe Ile Ala Glu Pro Leu Leu Gln Cys Ala Gly Asn Met His 210 215 220	734
att tat agc gca aga tat tta aaa caa gcc gtt tta ttg tgc aag caa Ile Tyr Ser Ala Arg Tyr Leu Lys Gln Ala Val Leu Leu Cys Lys Gln 225 230 235	782
aaa aac atc cac att att ttt gat gaa atc gct acc ggg ttt ggg cgc Lys Asn Ile His Ile Ile Phe Asp Glu Ile Ala Thr Gly Phe Gly Arg 240 245 250	830
aca ggg agc atg ttt gct tat gaa caa tgc gaa att aag ccg gat ttt Thr Gly Ser Met Phe Ala Tyr Glu Gln Cys Glu Ile Lys Pro Asp Phe 255 260 265	878
tta tgc ttg tct aag ggg att agt ggg ggg tat ttg cct tta agc gca Leu Cys Leu Ser Lys Gly Ile Ser Gly Gly Tyr Leu Pro Leu Ser Ala 270 275 280 285	926
cta tta acc cat aat gaa atc tat aac caa ttt tac gcc ccc tat gaa Leu Leu Thr His Asn Glu Ile Tyr Asn Gln Phe Tyr Ala Pro Tyr Glu 290 295 300	974
gaa aat aaa gcg ttt ttg cat tcg cac agc tac aca gga aac gct ttg Glu Asn Lys Ala Phe Leu His Ser His Ser Tyr Thr Gly Asn Ala Leu 305 310 315	1022
gca tgc gca tgc gcg aac gct acg ctg gat att ttt gaa aaa gaa aat Ala Cys Ala Cys Ala Asn Ala Thr Leu Asp Ile Phe Glu Lys Glu Asn 320 325 330	1070
gtt att gaa aag aac aag gct tta agc ggg ttt att ttt aat acg ctc Val Ile Glu Lys Asn Lys Ala Leu Ser Gly Phe Ile Phe Asn Thr Leu 335 340 345	1118
caa aac gca tta aaa ccc ttg atg gag caa caa gtg gtg tct gat tta Gln Asn Ala Leu Lys Pro Leu Met Glu Gln Gln Val Val Ser Asp Leu 350 355 360 365	1166
agg cat ttg ggc atg gtc ttt gcc ttt gaa gtc ttt att caa acc aaa Arg His Leu Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys 370 375 380	1214
gag cgt ttg agt ttg gcg gtt ttt aaa aaa act cta aaa aaa ggc ctg Glu Arg Leu Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu 385 390 395	1262
tta tta cgc cct tta aac aac acc att tac ctc atg ccc cct tac att Leu Leu Arg Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Pro Tyr Ile 400 405 410	1310
atc acg cat gaa gaa gtc aaa aag gcg gtt gcg ggg cta gtg gaa att Ile Thr His Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile 415 420 425	1358



Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys Glu Arg Leu  
 370 375 380  
 Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu Leu Leu Arg  
 385 390 395 400  
 Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Pro Tyr Ile Ile Thr His  
 405 410 415  
 Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile Leu Asp Glu  
 420 425 430  
 Leu Arg Lys Gly  
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<210> 109  
 <211> 360  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (82)...(294)

<400> 109

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 aaaagaaaaa aaggaaacaa c atg gga aaa atg aaa caa gaa aca gcg att 111  
 Met Gly Lys Met Lys Gln Glu Thr Ala Ile  
 1 5 10  
 gac tat gaa aaa tta gcg aat cat tgg aat aat aat gat gaa aac agc 159  
 Asp Tyr Glu Lys Leu Ala Asn His Trp Asn Asn Asn Asp Glu Asn Ser  
 15 20 25  
 gaa gca cta aac gct ttt gca gac gct tac ctt tat aaa cat gag aaa 207  
 Glu Ala Leu Asn Ala Phe Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys  
 30 35 40  
 aag agt caa aag att cgg gca ata gag ata agt tct cta aac aaa gcc 255  
 Lys Ser Gln Lys Ile Arg Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala  
 45 50 55  
 tgc atg gga gaa ttt tac cac aaa aac cca aaa tta ttt taataacgat 304  
 Cys Met Gly Glu Phe Tyr His Lys Asn Pro Lys Leu Phe  
 60 65 70  
 cgctccaagg aaccaacgcc ccatgacctc aagaaaagag aatagcttga atcggt 360

<210> 110  
 <211> 71  
 <212> PRT  
 <213> Helicobacter pylori

<400> 110

Met Gly Lys Met Lys Gln Glu Thr Ala Ile Asp Tyr Glu Lys Leu Ala  
 1 5 10 15  
 Asn His Trp Asn Asn Asn Asp Glu Asn Ser Glu Ala Leu Asn Ala Phe  
 20 25 30  
 Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys Lys Ser Gln Lys Ile Arg  
 35 40 45  
 Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala Cys Met Gly Glu Phe Tyr  
 50 55 60  
 His Lys Asn Pro Lys Leu Phe

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<220>  
<221> CDS  
<222> (62)...(1255)
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-122-



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Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn	
		195					200					205				
tat	caa	aat	tta	agc	ttg	act	gat	aaa	ggc	aat	atg	ttt	tta	gtg	gct	733
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala	
	210					215					220					
aag	ttt	ttt	aaa	gat	agt	gct	tta	ctt	ggt	aat	att	gct	agg	ttt	gaa	781
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu	
225					230					235					240	
atg	aaa	aag	ata	gat	gat	agt	gtt	aaa	aat	tct	aac	cca	caa	gac	aat	829
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn	
				245					250					255		
tta	tta	gac	aaa	caa	gtt	tgg	ctc	aat	ctt	tta	gag	cat	tta	aaa	aga	877
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg	
			260					265					270			
ctt	gaa	gag	gaa	aat	tat	tgt	ttt	gct	aag	aaa	cga	aaa	gaa	ttc	tta	925
Leu	Glu	Glu	Glu	Asn	Tyr	Cys	Phe	Ala	Lys	Lys	Arg	Lys	Glu	Phe	Leu	
		275					280					285				
gag	act	aga	gcg	atg	gag	cta	tca	aaa	gat	tta	aaa	ttt	tta	aca	cag	973
Glu	Thr	Arg	Ala	Met	Glu	Leu	Ser	Lys	Asp	Leu	Lys	Phe	Leu	Thr	Gln	
	290					295					300					
gct	aat	gaa	aat	gat	ttg	ccc	att	tat	gaa	aga	ggg	caa	agg	gat	aaa	1021
Ala	Asn	Glu	Asn	Asp	Leu	Pro	Ile	Tyr	Glu	Arg	Gly	Gln	Arg	Asp	Lys	
305					310					315					320	
atc	att	aaa	cgc	tgt	gaa	aaa	tcg	ctt	aac	ttt	ttg	cag	aaa	gaa	tta	1069
Ile	Ile	Lys	Arg	Cys	Glu	Lys	Ser	Leu	Asn	Phe	Leu	Gln	Lys	Glu	Leu	
				325					330					335		
caa	tgc	ttt	aaa	acc	tta	ttg	aaa	agt	gca	agt	ata	gct	tta	gaa	aac	1117
Gln	Cys	Phe	Lys	Thr	Leu	Leu	Lys	Ser	Ala	Ser	Ile	Ala	Leu	Glu	Asn	
			340					345					350			
ttg	caa	aat	aac	cat	caa	atc	aca	gcc	gtt	aca	caa	gac	acg	caa	gaa	1165
Leu	Gln	Asn	Asn	His	Gln	Ile	Thr	Ala	Val	Thr	Gln	Asp	Thr	Gln	Glu	
		355				360						365				
aac	aca	aac	gcg	ctc	aaa	aat	act	act	caa	gat	ttt	aac	aaa	act	acc	1213
Asn	Thr	Asn	Ala	Leu	Lys	Asn	Thr	Thr	Gln	Asp	Phe	Asn	Lys	Thr	Thr	
	370					375					380					
aat	gaa	cca	aca	aac	cct	aac	aat	aac	tat	gga	atg	gat	ttt			1255
Asn	Glu	Pro	Thr	Asn	Pro	Asn	Asn	Asn	Tyr	Gly						

<213> Helicobacter pylori

<400> 112

Arg	His	Arg	Asn	Arg	Ala	Arg	Cys	Thr	Arg	Lys	Gln	Ala	Arg	Asn	Asn
1				5					10					15	
Lys	Ser	Phe	Arg	His	Glu	Asn	Tyr	Phe	Tyr	Lys	Val	Leu	Gly	Ser	Ala
			20					25					30		
Thr	Ser	Gln	Ile	Glu	Ser	Leu	Lys	Lys	Arg	Glu	Asn	Ala	Leu	Phe	Asp
		35					40					45			
His	Leu	Asp	Ser	Leu	Lys	Ser	Leu	Leu	Glu	Lys	Thr	His	Trp	Glu	Lys
	50					55					60				
Glu	Lys	Phe	Thr	Pro	Pro	Ile	Asn	Glu	Lys	Glu	Leu	Asn	Arg	Gln	Leu
65					70					75					80
Lys	Glu	Val	Arg	Trp	Phe	Asn	Lys	Glu	Thr	Pro	Thr	Ser	Lys	Asn	Thr
				85					90					95	
Tyr	Lys	Lys	Ile	Gln	Lys	Leu	Ala	Val	Tyr	Lys	Ser	Pro	Leu	Ile	Lys
			100					105					110		
Asp	Tyr	Leu	Tyr	Thr	Ile	Lys	Lys	Leu	Phe	Ala	Thr	Gln	Lys	Lys	Ile
	115						120					125			
Ile	Asp	Leu	Glu	Lys	Asn	Tyr	Lys	Asp	Leu	Arg	Ala	Leu	Lys	Glu	Glu
130						135						140			
Phe	Ser	Lys	Asp	Leu	Glu	Thr	Asp	Leu	Ser	His	Ser	Lys	Lys	Arg	Phe
145					150					155					160
Glu	Leu	Tyr	Thr	Arg	Leu	Lys	Ser	Met	Ser	Lys	Val	Phe	Ile	Ser	Lys
				165					170					175	
Ser	Ile	Val	Lys	Asn	Leu	Glu	Lys	Ile	Ala	Leu	Asp	Phe	Lys	Ser	Asp
			180					185					190		
Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn
	195						200					205			
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala
	210					215					220				
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu
225					230					235					240
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn
				245					250					255	
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg
			260					265					270		
Leu	Glu	Glu	Glu	Asn	Tyr	Cys	Phe	Ala	Lys	Lys	Arg	Lys	Glu	Phe	Leu
			275				280					285			
Glu	Thr	Arg	Ala	Met	Glu	Leu	Ser	Lys	Asp	Leu	Lys	Phe	Leu	Thr	Gln
	290					295					300				
Ala	Asn	Glu	Asn	Asp	Leu	Pro	Ile	Tyr	Glu	Arg	Gly	Gln	Arg	Asp	Lys
305					310					315					320
Ile	Ile	Lys	Arg	Cys	Glu	Lys	Ser	Leu	Asn	Phe	Leu	Gln	Lys	Glu	Leu
				325					330					335	
Gln	Cys	Phe	Lys	Thr	Leu	Leu	Lys	Ser	Ala	Ser	Ile	Ala	Leu	Glu	Asn
			340					345					350		
Leu	Gln	Asn	Asn	His	Gln	Ile	Thr	Ala	Val	Thr	Gln	Asp	Thr	Gln	Glu
		355					360					365			
Asn	Thr	Asn	Ala	Leu	Lys	Asn	Thr	Thr	Gln	Asp	Phe	Asn	Lys	Thr	Thr
	370					375					380				
Asn	Glu	Pro	Thr	Asn	Pro	Asn	Asn	Asn	Tyr	Gly	Met	Asp	Phe		
385					390					395					

<210> 113

<211> 630

<212> DNA

<213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (105)...(518)

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<400> 113
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ctttcataga aagtatttta acctcttttt gttaaaatag gtct atg aaa aaa att      116
                               Met Lys Lys Ile
                               1

gat gat atg aga cac gga aga cat tgt gtt ttt tta atg cat gtg cat      164
Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His Val His
 5                               10                               15                               20

ttt gta ttt gtt act aaa tac agg cgt tca gca ttc aat aag gaa gtg      212
Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe Asn Lys Glu Val
                               25                               30                               35

ata gat ttt tta gga tcg gtg ttt gcc aaa gtg tgt aag gac ttt gag      260
Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys Lys Asp Phe Glu
                               40                               45                               50

agc gaa ttg gta gaa ttt gat ggg gag agc gat cat gtg cat ttg ctt      308
Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His Val His Leu Leu
                               55                               60                               65

atc aac tac cct cca aaa gtg agc gtg agt aag tta gtt aat tct tta      356
Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu Val Asn Ser Leu
                               70                               75                               80

aaa ggc gtt agc agt cgt ttg act aga caa cac cat ttc aaa agc gtt      404
Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His Phe Lys Ser Val
 85                               90                               95                               100

gaa gct agt ttg tgg ggg aag cat tta tgg tcg cct agt tat ttc gct      452
Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro Ser Tyr Phe Ala
                               105                               110                               115

ggg agt tgt ggg gac gcg cct tta gag atg att aag caa tac ata caa      500
Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys Gln Tyr Ile Gln
                               120                               125                               130

gat caa gaa aca ccg cat taaattagct aactttgatt tttaagtaga      548
Asp Gln Glu Thr Pro His
                               135

acgcgctaaa aagcgaatgg atctaagtga aacaatgttc aaatagccta acggcctaaac      608
gcttacatct ccgccctaaa gg      630

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<210> 114  
 <211> 138  
 <212> PRT  
 <213> Helicobacter pylori

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<400> 114
Met Lys Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu
 1                               5                               10                               15
Met His Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe
 20                               25                               30

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[illegible]

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<220>
<221> CDS
<222> (101)...(1000)
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-126-



Phe Gln Gly Met Asp Ala Cys Val Pro Val Gly Thr Thr Gly Glu Ser  
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Ala Thr Leu Thr His Lys Glu His Met Arg Cys Ile Glu Ile Ala Ile  
50 55 60  
Glu Thr Cys Lys Asn Thr Lys Thr Pro Ser Asn Ser Arg Met Lys Val  
65 70 75 80  
Leu Ala Gly Val Gly Ser Asn Ala Thr Ser Glu Ser Leu Ser Leu Ala  
85 90 95  
Lys Phe Ala Gln Lys Ile Gly Ala Asp Ala Ile Leu Cys Val Ser Pro  
100 105 110  
Tyr Tyr Asn Arg Pro Thr Gln Gln Gly Leu Phe Glu His Tyr Lys Thr  
115 120 125  
Ile Ala Gln Ser Val Glu Ile Pro Val Met Leu Tyr Asp Val Pro Ser  
130 135 140  
Arg Thr Gly Val Ser Ile Glu Val Pro Thr Ala Leu Lys Leu Phe Arg  
145 150 155 160  
Glu Val Pro Asn Ile Lys Ala Ile Lys Glu Ala Ser Gly Ser Leu Lys  
165 170 175  
Arg Val Thr Glu Leu His Tyr Tyr Glu Lys Asp Phe Lys Ile Phe Ser  
180 185 190  
Gly Glu Asp Ser Leu Asn His Ser Ile Met Phe Ser Gly Gly Cys Gly  
195 200 205  
Val Ile Ser Val Thr Gly Asn Leu Met Pro Asn Leu Ile Ser Gln Met  
210 215 220  
Val Asn Cys Ala Leu Lys Gln Lys Tyr Gln Gln Ala Leu Glu Ile Gln  
225 230 235 240  
Asn Lys Leu Phe Cys Leu His Gln Ala Leu Phe Val Glu Thr Asn Pro  
245 250 255  
Ile Pro Ile Lys Met Ala Met His Leu Ala Gly Leu Ile Glu Asn Pro  
260 265 270  
Ser Tyr Arg Leu Pro Leu Val Ala Pro Ser Lys Glu Thr Ile Gln Leu  
275 280 285  
Leu Glu Lys Thr Leu Gln Gln Tyr Glu Val Ile Ala  
290 295 300

<210> 117  
<211> 1709  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (68)...(1624)

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ttaaaaa atg ctt ttg atc gtt ttt ttt aaa ttt tat ttt caa tat tca 109  
Met Leu Leu Ile Val Phe Phe Lys Phe Tyr Phe Gln Tyr Ser  
1 5 10  
att aaa aaa aaa tca ttt tat ttt att ttt gtt ata att caa gct att 157  
Ile Lys Lys Lys Ser Phe Tyr Phe Ile Phe Val Ile Ile Gln Ala Ile 30  
15 20 25  
ttt att ttc aat cta agg agg tgt cgc atg gac aat caa aag ata acg 205  
Phe Ile Phe Asn Leu Arg Arg Cys Arg Met Asp Asn Gln Lys Ile Thr 45  
35 40  
cat caa aat atc acg caa aaa caa ggc gag ctt aaa aga gac atg aaa 253



[illegible]







gtt acg caa ggc att gtt tca gcg ctc aat aaa agc ggg att ggg atc Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly Ile Gly Ile 100 105 110 115	574
aac agc tat gag aat ttc att caa aca gac gct tcc atc aat cct gga Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile Asn Pro Gly 120 125 130	622
aat tcc ggc ggc gct tta att gat agc cgt gga ggg tta gtg ggg att Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu Val Gly Ile 135 140 145	670
aat acc gct att atc tct aaa act ggg ggc aac cac ggc att ggc ttt Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly Ile Gly Phe 150 155 160	718
gcc atc cct tct aac atg gtt aaa gat act gta acc caa ctc atc aaa Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln Leu Ile Lys 165 170 175	766
acc ggt aag att gaa aga ggt tac ttg ggc gtg ggc ttg caa gat ttg Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu Gln Asp Leu 180 185 190 195	814
agt ggc gat ttg caa aat tct tat gac aac aaa gaa ggg gcg gta gtc Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly Ala Val Val 200 205 210	862
att agc gta gaa aaa gac tct ccg gct aaa aaa gca ggg att ttg gtg Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly Ile Leu Val 215 220 225	910
tgg gat ttg atc acc gaa gtc aat ggg aaa aag gtt aaa aac acg aat Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys Asn Thr Asn 230 235 240	958
gag tta aga aat cta atc ggc tcc atg cta ccc aat caa aga gta acc Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln Arg Val Thr 245 250 255	1006
tta aaa gtc att aga gac aaa aaa gaa cgc gct ttc acc ctc act cta Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr Leu Thr Leu 260 265 270 275	1054
gct gaa agg aaa aac cct aac aaa aaa gaa acc att tct gct caa aac Ala Glu Arg Lys Asn Pro Asn Lys Lys Glu Thr Ile Ser Ala Gln Asn 280 285 290	1102
ggc gcg caa ggc caa ttg aac ggg ctt caa gta gaa gat tta act caa Gly Ala Gln Gly Gln Leu Asn Gly Leu Gln Val Glu Asp Leu Thr Gln 295 300 305	1150
gaa acc aaa agg tct atg cgt ttg agc gat gat gtt caa ggg gtt tta Glu Thr Lys Arg Ser Met Arg Leu Ser Asp Asp Val Gln Gly Val Leu 310 315 320	1198
gtc tct caa gtg aat gaa aat tcc cca gca gag caa gcc gga ttt agg Val Ser Gln Val Asn Glu Asn Ser Pro Ala Glu Gln Ala Gly Phe Arg 325 330 335	1246

caa ggt aac att atc aca aaa att gaa gag gtt gaa gtt aaa agc gtt	1294
Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val Lys Ser Val	
340 345 350 355	
gcg gat ttt aac cat gct tta gaa aag tat aaa ggc aaa ccc aaa cga	1342
Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg	
360 365 370	
ttc tta gtt tta gac ttg aat caa ggt tat agg atc att ttg gtg aaa	1390
Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys	
375 380 385	
tgataggggt gggtcggttag tcgcatgtct ttgattagag tgaatgggga agcttttaaa	1450
ctctcttttag aaagtttaga agaagaccct tttgaaacta aagaaacgct agaaacgctt	1510
atcaaacaaa cgagcgttg	1529

<210> 120  
 <211> 387  
 <212> PRT  
 <213> Helicobacter pylori

<400> 120

Met Ile Pro Lys Glu Arg Met Glu Arg Ala Leu Gly Ser Gly Val Ile	
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Ile Ser Lys Asp Gly Tyr Ile Val Thr Asn Asn His Val Ile Asp Gly	
20 25 30	
Ala Asp Lys Ile Lys Val Thr Ile Pro Gly Ser Asn Lys Glu Tyr Ser	
35 40 45	
Ala Thr Leu Val Gly Thr Asp Ser Glu Ser Asp Leu Ala Val Ile Arg	
50 55 60	
Ile Thr Lys Asp Asn Leu Pro Thr Ile Lys Phe Ser Asp Ser Asn Asp	
65 70 75 80	
Ile Ser Val Gly Asp Leu Val Phe Ala Ile Gly Asn Pro Phe Gly Val	
85 90 95	
Gly Glu Ser Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly	
100 105 110	
Ile Gly Ile Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile	
115 120 125	
Asn Pro Gly Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu	
130 135 140	
Val Gly Ile Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly	
145 150 155 160	
Ile Gly Phe Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln	
165 170 175	
Leu Ile Lys Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu	
180 185 190	
Gln Asp Leu Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly	
195 200 205	
Ala Val Val Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly	
210 215 220	
Ile Leu Val Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys	
225 230 235 240	
Asn Thr Asn Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln	
245 250 255	
Arg Val Thr Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr	
260 265 270	
Leu Thr Leu Ala Glu Arg Lys Asn Pro Asn Lys Lys Glu Thr Ile Ser	
275 280 285	

Ala Gln Asn Gly Ala Gln Gly Gln Leu Asn Gly Leu Gln Val Glu Asp  
 290 295 300  
 Leu Thr Gln Glu Thr Lys Arg Ser Met Arg Leu Ser Asp Asp Val Gln  
 305 310 315 320  
 Gly Val Leu Val Ser Gln Val Asn Glu Asn Ser Pro Ala Glu Gln Ala  
 325 330 335  
 Gly Phe Arg Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val  
 340 345 350  
 Lys Ser Val Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys  
 355 360 365  
 Pro Lys Arg Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile  
 370 375 380  
 Leu Val Lys  
 385

<210> 121  
 <211> 990  
 <212> DNA  
 <213> Helicobacter pylori  
 <220>  
 <221> CDS  
 <222> (39)...(902)

<400> 121  
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 Met Ser Lys Ser Leu Tyr  
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 caa act tta aat gtg agc gaa aac gcc agc caa gat gaa atc aaa aaa 104  
 Gln Thr Leu Asn Val Ser Glu Asn Ala Ser Gln Asp Glu Ile Lys Lys  
 10 15 20  
 tcc tac cgc cgt tta gcc cga caa tac cac ccg gat ttg aat aaa acc 152  
 Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His Pro Asp Leu Asn Lys Thr  
 25 30 35  
 aaa gaa gcc gaa gag aaa ttc aaa gaa atc aac gcc gct tat gaa att 200  
 Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile Asn Ala Ala Tyr Glu Ile  
 40 45 50  
 ttg agc gat gaa gaa aaa cgc cgc caa tac gat cag ttt ggc gat aac 248  
 Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr Asp Gln Phe Gly Asp Asn  
 55 60 65 70  
 atg ttt ggc ggg cag aat ttc agc gat ttt gcc aga agc cgt ggt cct 296  
 Met Phe Gly Gly Gln Asn Phe Ser Asp Phe Ala Arg Ser Arg Gly Pro  
 75 80 85  
 agt gaa gat tta gac gat att tta agc tct att ttt ggg aaa gga ggc 344  
 Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser Ile Phe Gly Lys Gly Gly  
 90 95 100  
 ttt tcg caa aga ttt tct caa aac tcg caa ggc ttt tct ggc ttt aat 392  
 Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln Gly Phe Ser Gly Phe Asn  
 105 110 115  
 ttt tcc aat ttc gcc cct gaa aat tta gac ata acc gcc gct tta aat 440  
 Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp Ile Thr Ala Ala Leu Asn

120	125	130	
gtc tct gtt tta gac acc ctt tta ggc aat aaa aaa caa gtg agc atc Val Ser Val Leu Asp Thr Leu Leu Gly Asn Lys Lys Gln Val Ser Ile 135 140 145 150			488
aat aat gag act ttt agc ctt aaa atc cct att ggc gtg gaa gag ggc Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro Ile Gly Val Glu Glu Gly 155 160 165			536
gaa aag att agg gtt cgc aac aag ggg aaa acg ggg cga acg act agg Glu Lys Ile Arg Val Arg Asn Lys Gly Lys Thr Gly Arg Thr Thr Arg 170 175 180			584
ggc gat ttg ctc tta gag atc cat att gaa gaa gat gaa atg tat agg Gly Asp Leu Leu Leu Glu Ile His Ile Glu Glu Asp Glu Met Tyr Arg 185 190 195			632
cgc gag aaa gat gat att acc caa atc ttt gat tta ccc tta aaa acg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe Asp Leu Pro Leu Lys Thr 200 205 210			680
gct ctt ttt gga ggg aaa att gaa atc gct act tgg cat aaa acc tta Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala Thr Trp His Lys Thr Leu 215 220 225 230			728
acc cta acc att ccc cct aac acc aaa gcg atg caa aaa ttc cgc att Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala Met Gln Lys Phe Arg Ile 235 240 245			776
aaa gaa aaa ggg atc aaa aac aga aaa act tcg cat gtg ggg gat ttg Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr Ser His Val Gly Asp Leu 250 255 260			824
tat ttg cag gct cgt ttg att ttg cct aaa act gaa acg ctt tct aat Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys Thr Glu Thr Leu Ser Asn 265 270 275			872
gag ttg aaa gcg tta tta gaa aaa gaa ttg taaggaggaa tcgtgtgcga Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu 280 285			922
ttatgatgaa ccgctttatt taatcagcgt cgtggctaaa atcttaggcg tgcaccctca aaccttgc			982 990

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 <212> PRT  
 <213> Helicobacter pylori

<400> 122

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Gln Asp Glu Ile Lys Lys Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His 20 25 30	
Pro Asp Leu Asn Lys Thr Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile 35 40 45	
Asn Ala Ala Tyr Glu Ile Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr 50 55 60	

Asp Gln Phe Gly Asp Asn Met Phe Gly Gly Gln Asn Phe Ser Asp Phe  
65 70 75 80  
Ala Arg Ser Arg Gly Pro Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser  
85 90 95  
Ile Phe Gly Lys Gly Gly Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln  
100 105 110  
Gly Phe Ser Gly Phe Asn Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp  
115 120 125  
Ile Thr Ala Ala Leu Asn Val Ser Val Leu Asp Thr Leu Leu Gly Asn  
130 135 140  
Lys Lys Gln Val Ser Ile Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro  
145 150 155 160  
Ile Gly Val Glu Glu Gly Glu Lys Ile Arg Val Arg Asn Lys Gly Lys  
165 170 175  
Thr Gly Arg Thr Thr Arg Gly Asp Leu Leu Leu Glu Ile His Ile Glu  
180 185 190  
Glu Asp Glu Met Tyr Arg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe  
195 200 205  
Asp Leu Pro Leu Lys Thr Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala  
210 215 220  
Thr Trp His Lys Thr Leu Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala  
225 230 235 240  
Met Gln Lys Phe Arg Ile Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr  
245 250 255  
Ser His Val Gly Asp Leu Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys  
260 265 270  
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275 280 285

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<222> (113)...(1285)

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cgaaaaattt aaacaccctt acgaattttt acgaattgat tttatttaaa aa atg agc 118  
Met Ser  
1  
  
ctg act tcg ctt tta aac cca aaa agc cta gaa gat ttt tta ggc caa 166  
Leu Thr Ser Leu Leu Asn Pro Lys Ser Leu Glu Asp Phe Leu Gly Gln  
5 10 15  
  
gag cat tta gta ggg aaa gac gcc ccc tta ttt aaa gcc cta caa tcc 214  
Glu His Leu Val Gly Lys Asp Ala Pro Leu Phe Lys Ala Leu Gln Ser  
20 25 30  
  
aaa cac ttc ccc cat gcc ttt ttc tat ggc cct cct ggc gtg ggt aaa 262  
Lys His Phe Pro His Ala Phe Phe Tyr Gly Pro Pro Gly Val Gly Lys  
35 40 45 50  
  
aca agc ctg gct caa atc atc gcc tat atg cta gag cgc ccc att ctt 310  
Thr Ser Leu Ala Gln Ile Ile Ala Tyr Met Leu Glu Arg Pro Ile Leu  
55 60 65





295										300										305										
gtg	att	tat	ctg	gct	tgt	tcg	ccc	aag	tct	aac	acg	gct	tat	aga	gcg		1078													
Val	Ile	Tyr	Leu	Ala	Cys	Ser	Pro	Lys	Ser	Asn	Thr	Ala	Tyr	Arg	Ala															
			310						315						320															
atc	aat	cag	gct	ttg	gat	tgc	gtt	caa	aaa	ggc	tca	ctc	tac	cct	att		1126													
Ile	Asn	Gln	Ala	Leu	Asp	Cys	Val	Gln	Lys	Gly	Ser	Leu	Tyr	Pro	Ile															
			325						330						335															
cct	aaa	cac	ctg	ctg	cct	aac	gct	aaa	gat	tac	ctt	tac	ccg	cat	gat		1174													
Pro	Lys	His	Leu	Leu	Pro	Asn	Ala	Lys	Asp	Tyr	Leu	Tyr	Pro	His	Asp															
			340						345						350															
tat	aac	ggc	tat	gtc	aaa	caa	gat	tat	ttg	gaa	aaa	ccc	cta	gat	ttg		1222													
Tyr	Asn	Gly	Tyr	Val	Lys	Gln	Asp	Tyr	Leu	Glu	Lys	Pro	Leu	Asp	Leu															
			355						360						365															
gtt	tct	tct	caa	ggc	ata	gga	ttt	gaa	aaa	acc	ctt	tta	gaa	tgg	ctt		1270													
Val	Ser	Ser	Gln	Gly	Ile	Gly	Phe	Glu	Lys	Thr	Leu	Leu	Glu	Trp	Leu															
			375						380						385															
gat	aag	ata	aga	aat	tgatcttata	agttacatta	aaatgcgaca	atggtaataa									1325													
Asp	Lys	Ile	Arg	Asn																										
			390																											
aaaatcaata tttttggatt gaatt																1350														
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1				5					10					15																
Gly	Gln	Glu	His	Leu	Val	Gly	Lys	Asp	Ala	Pro	Leu	Phe	Lys	Ala	Leu															
			20						25						30															
Gln	Ser	Lys	His	Phe	Pro	His	Ala	Phe	Phe	Tyr	Gly	Pro	Pro	Gly	Val															
			35						40						45															
Gly	Lys	Thr	Ser	Leu	Ala	Gln	Ile	Ile	Ala	Tyr	Met	Leu	Glu	Arg	Pro															
			50						55						60															
Ile	Leu	Leu	Phe	Asn	Ala	Thr	Asp	Phe	Lys	Leu	Glu	Asp	Leu	Arg	Leu															
			65						70						75															
Lys	Leu	Lys	Asn	Tyr	Gln	Asn	Thr	Leu	Leu	Lys	Pro	Val	Val	Phe	Ile															
			85						90						95															
Asp	Glu	Thr	His	Arg	Leu	Asn	Lys	Thr	Gln	Gln	Glu	Phe	Leu	Leu	Pro															
			100						105						110															
Ile	Met	Glu	Lys	Asp	His	Ala	Leu	Ile	Leu	Gly	Ala	Ser	Thr	Gln	Asp															
			115						120						125															
Pro	Asn	Tyr	Ser	Leu	Ser	His	Ala	Ile	Arg	Ser	Arg	Ser	Phe	Ile	Phe															
			130						135						140															
Glu	Leu	Thr	Pro	Leu	Asn	Lys	Ser	Asp	Leu	Asp	Arg	Leu	Cys	Ala	Lys															
			145						150						155															
Ala	Leu	Thr	Leu	Leu	Lys	Lys	Gln	Ile	Glu	Pro	Gly	Ala	Lys	Thr	Tyr															
			165						170						175															
Leu	Leu	Asn	Asn	Ser	Ala	Gly	Asp	Ala	Arg	Ala	Leu	Leu	Asn	Leu	Leu															
			180						185						190															
Asp	Leu	Ser	Ala	Lys	Ile	Glu	Asp	Pro	Ile	Thr	Leu	Lys	Thr	Leu	Gln															

Ser	Leu	Arg	Pro	His	Ser	Leu	Asn	Asp	Gly	Ser	Tyr	Ser	Asp	Asp	Thr
210						215					220				
His	Tyr	Asn	Leu	Thr	Ser	Ala	Leu	Ile	Lys	Ser	Leu	Arg	Gly	Ser	Asp
225					230					235					240
Glu	Asn	Ala	Ser	Ile	Tyr	Tyr	Leu	Ala	Arg	Leu	Ile	Ala	Gly	Gly	Glu
				245					250					255	
Asn	Pro	Glu	Phe	Ile	Ala	Arg	Arg	Leu	Val	Ile	Phe	Ala	Ser	Glu	Asp
			260					265					270		
Ile	Gly	Asn	Ala	Asn	Pro	Asn	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Cys	Leu
		275					280						285		
Phe	Ala	Val	Lys	Gln	Ile	Gly	Tyr	Pro	Glu	Ala	Arg	Ile	Ile	Leu	Ser
290					295						300				
Gln	Cys	Val	Ile	Tyr	Leu	Ala	Cys	Ser	Pro	Lys	Ser	Asn	Thr	Ala	Tyr
305					310					315					320
Arg	Ala	Ile	Asn	Gln	Ala	Leu	Asp	Cys	Val	Gln	Lys	Gly	Ser	Leu	Tyr
				325					330					335	
Pro	Ile	Pro	Lys	His	Leu	Leu	Pro	Asn	Ala	Lys	Asp	Tyr	Leu	Tyr	Pro
			340					345					350		
His	Asp	Tyr	Asn	Gly	Tyr	Val	Lys	Gln	Asp	Tyr	Leu	Glu	Lys	Pro	Leu
		355					360					365			
Asp	Leu	Val	Ser	Ser	Gln	Gly	Ile	Gly	Phe	Glu	Lys	Thr	Leu	Leu	Glu
370					375						380				
Trp	Leu	Asp	Lys	Ile	Arg	Asn									
385					390										

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attttatggt	cttta	atg ggg ttt	tat gca gga	ttg aac gcg	ctt gat tat										111
		Met Gly Phe Tyr	Ala Gly Leu	Asn Ala Leu	Asp Tyr										
		1		5											
gac acc ata	gac cca	aaa tac	tac aag	tat atc	aag tat	tat tat	aaa gcc								159
Asp Thr Ile	Asp Pro	Lys Tyr	Tyr Lys	Tyr Ile	Lys Tyr	Tyr Lys	Ala								
	15			20			25								
tat gag gat	aaa gaa	gtt gaa	gaa ttg	atc aga	gac tta	aaa agg	gcg								207
Tyr Glu Asp	Lys Glu	Val Glu	Glu Leu	Ile Arg	Asp Leu	Lys Arg	Ala								
	30		35			40									
aac gct aaa	agc ggg	ctt att	tta ggg	atc aat	acc ggg	ttt ttt	tac								255
Asn Ala Lys	Ser Gly	Leu Ile	Leu Gly	Ile Asn	Thr Gly	Phe Phe	Tyr								
	45		50		55		60								
aat cat gaa	atc atg	gtt aga	act aat	agc tct	agc atc	acg ggg	aat								303
Asn His Glu	Ile Met	Val Arg	Thr Asn	Ser Ser	Ser Ile	Thr Gly	Asn								
	65			70			75								
att tta aat	tat ttg	ttc gct	tac ggc	ttg cgt	ttt ggc	tat caa	act								351
Ile Leu Asn	Tyr Leu	Phe Ala	Tyr Gly	Leu Arg	Phe Gly	Tyr Gln	Thr								



Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly Arg Arg Ile Tyr  
 100 105 110  
 Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly Phe Gly Asp Val  
 115 120 125  
 Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu Leu Asp Phe Pro  
 130 135 140  
 Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly Tyr Met Gly Leu  
 145 150 155 160  
 Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr Ala Glu Trp Gly  
 165 170 175  
 Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu Glu Lys Asn Arg  
 180 185 190  
 Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro Phe Leu Gln Ser  
 195 200 205  
 Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala Asn Ile Gly Tyr  
 210 215 220  
 Gln Tyr Val Phe  
 225

<210> 127  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (89)...(1096)

<400> 127

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tccttaacga attagaaagt tatcatta atg aaa gaa cgg ata gtc aat tta	112
Met Lys Glu Arg Ile Val Asn Leu	
1 5	
gaa act ttg gat ttt gaa att tct caa gaa gtg agt ttg cgc cct agt	160
Glu Thr Leu Asp Phe Glu Ile Ser Gln Glu Val Ser Leu Arg Pro Ser	
10 15 20	
ctt tgg gaa gat ttt atc ggt caa gaa aag att aaa agc aat ttg caa	208
Leu Trp Glu Asp Phe Ile Gly Gln Glu Lys Ile Lys Ser Asn Leu Gln	
25 30 35 40	
att tct att tgc gcg gct aaa aaa cgc caa gaa agt ttg gat cac atg	256
Ile Ser Ile Cys Ala Ala Lys Lys Arg Gln Glu Ser Leu Asp His Met	
45 50 55	
ctt ttt ttt ggc cgc ccc ggt ttg ggt aaa act tca atc agc cat atc	304
Leu Phe Phe Gly Pro Pro Gly Leu Gly Lys Thr Ser Ile Ser His Ile	
60 65 70	
atc gct aaa gaa atg gaa acc aat atc aag atc acc gcc gct ccc atg	352
Ile Ala Lys Glu Met Glu Thr Asn Ile Lys Ile Thr Ala Ala Pro Met	
75 80 85	
ata gaa aaa agc ggt gat tta gcc gcc att ttg acc aat ttg caa gct	400
Ile Glu Lys Ser Gly Asp Leu Ala Ala Ile Leu Thr Asn Leu Gln Ala	
90 95 100	
aaa gac att ctt ttt att gat gaa atc cac cgg ctc agc cca gcg att	448



aataacgata aaatttttaaa ggggtgtaaaa gtagattgtt atgtt

1171

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<211> 336  
<212> PRT  
<213> Helicobacter pylori

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Met Lys Glu Arg Ile Val Asn Leu Glu Thr Leu Asp Phe Glu Ile Ser  
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Gln Glu Val Ser Leu Arg Pro Ser Leu Trp Glu Asp Phe Ile Gly Gln  
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Glu Lys Ile Lys Ser Asn Leu Gln Ile Ser Ile Cys Ala Ala Lys Lys  
35 40 45  
Arg Gln Glu Ser Leu Asp His Met Leu Phe Phe Gly Pro Pro Gly Leu  
50 55 60  
Gly Lys Thr Ser Ile Ser His Ile Ile Ala Lys Glu Met Glu Thr Asn  
65 70 75 80  
Ile Lys Ile Thr Ala Pro Met Ile Glu Lys Ser Gly Asp Leu Ala  
85 90 95  
Ala Ile Leu Thr Asn Leu Gln Ala Lys Asp Ile Leu Phe Ile Asp Glu  
100 105 110  
Ile His Arg Leu Ser Pro Ala Ile Glu Glu Val Leu Tyr Pro Ala Met  
115 120 125  
Glu Asp Phe Arg Leu Asp Ile Ile Ile Gly Ser Gly Pro Ala Ala Gln  
130 135 140  
Thr Ile Lys Ile Asp Leu Pro Pro Phe Thr Leu Ile Gly Ala Thr Thr  
145 150 155 160  
Arg Ala Gly Met Leu Ser Asn Pro Leu Arg Asp Arg Phe Gly Met Ser  
165 170 175  
Phe Arg Met Gln Phe Tyr Asn Pro Ser Glu Leu Ala Leu Ile Ile Lys  
180 185 190  
Lys Ala Ala Val Lys Leu Asn Gln Asp Ile Lys Gln Glu Ser Ala Asp  
195 200 205  
Glu Ile Ala Lys Arg Ser Arg Gly Thr Pro Arg Ile Ala Leu Arg Leu  
210 215 220  
Leu Lys Arg Val Arg Asp Phe Ala Leu Val Lys Asn Ser Ser Leu Met  
225 230 235 240  
Asp Leu Asn Ile Thr Leu His Ala Leu Asn Glu Leu Gly Val Asn Glu  
245 250 255  
Leu Gly Phe Asp Glu Ala Asp Leu Ala Tyr Leu Ser Leu Leu Ala Asn  
260 265 270  
Ala Gln Gly Lys Pro Val Gly Leu Asn Thr Ile Ala Ala Ser Met Arg  
275 280 285  
Glu Asp Glu Gly Thr Ile Glu Asp Val Ile Glu Pro Phe Leu Leu Ala  
290 295 300  
Asn Gly Tyr Leu Glu Arg Thr Ala Lys Gly Arg Ile Ala Thr Pro Lys  
305 310 315 320  
Thr His Glu Leu Leu Lys Ile Pro Thr Leu Asn Pro Gln Thr Leu Phe  
325 330 335

<210> 129  
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<220>  
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ccaattagca accgataaca acaccaaaga acacgacaaa gaaaaagaga atg ttt      116
                                   Met Phe
                                   1

gaa gat tta aaa ccg cat tta cag gaa tta aga aag cgt ttg atg gtt      164
Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu Met Val
      5                                10                                15

tct gta gga acg att cta gtg gcg ttt ttg ggg tgc ttt cat ttt tgg      212
Ser Val Gly Thr Ile Leu Val Ala Phe Leu Gly Cys Phe His Phe Trp
      20                                25                                30

aaa agt att ttt gaa ttt gtt aaa aat tcc tat aaa ggc acg ctc att      260
Lys Ser Ile Phe Glu Phe Val Lys Asn Ser Tyr Lys Gly Thr Leu Ile
      35                                40                                45                                50

cag ctc tcc cct att gaa ggg gtc atg gta gcg gtt aaa atc agt ttt      308
Gln Leu Ser Pro Ile Glu Gly Val Met Val Ala Val Lys Ile Ser Phe
                                   55                                60                                65

tca gcc gct atc gtc att tcc atg ccc att att ttt tgg caa tta tgg      356
Ser Ala Ala Ile Val Ile Ser Met Pro Ile Ile Phe Trp Gln Leu Trp
                                   70                                75                                80

ctc ttt atc gct cca ggg ctt tac aag aat gaa aaa aaa gtg att ttg      404
Leu Phe Ile Ala Pro Gly Leu Tyr Lys Asn Glu Lys Lys Val Ile Leu
                                   85                                90                                95

cct ttt gtg ttt ttt ggg agt ggg atg ttt ttg att ggg gcg gcg ttt      452
Pro Phe Val Phe Phe Gly Ser Gly Met Phe Leu Ile Gly Ala Ala Phe
      100                                105                                110

tct tat tat gtg gtg ttc cct ttc att att gaa tac tta gcc act ttt      500
Ser Tyr Tyr Val Val Phe Pro Phe Ile Ile Glu Tyr Leu Ala Thr Phe
      115                                120                                125                                130

ggg agc gat gtg ttt gcg gct aat att tct gcg tcc agt tac gtg agc      548
Gly Ser Asp Val Phe Ala Ala Asn Ile Ser Ala Ser Ser Tyr Val Ser
                                   135                                140                                145

ttt ttc acg cgc ttg att tta ggc ttt ggc gtg gcg ttt gaa ttg cct      596
Phe Phe Thr Arg Leu Ile Leu Gly Phe Gly Val Ala Phe Glu Leu Pro
                                   150                                155                                160

gtt ttg gcg tat ttt ttg gct aaa gtg ggc ttg att act gat gcg agc      644
Val Leu Ala Tyr Phe Leu Ala Lys Val Gly Leu Ile Thr Asp Ala Ser
                                   165                                170                                175

ttg aaa gcg tat ttt aaa tac gct att gta gtg att ttt att gta gca      692
Leu Lys Ala Tyr Phe Lys Tyr Ala Ile Val Val Ile Phe Ile Val Ala
      180                                185                                190

gcc att atc act ccc cct gat gtg gtg agt caa atc ttt atg gcg ttg      740
Ala Ile Ile Thr Pro Pro Asp Val Val Ser Gln Ile Phe Met Ala Leu
      195                                200                                205                                210

ccc tta gtg ggg ctt tat ggg ctt tct att tta atc gcc aaa atg gtc      788

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Pro	Leu	Val	Gly	Leu	Tyr	Gly	Leu	Ser	Ile	Leu	Ile	Ala	Lys	Met	Val	
			215						220					225		
aat	ccg	gct	ccc	aaa	gat	aac	gaa	aat	aac	aac	gaa	aat	aat	aac	gaa	836
Asn	Pro	Ala	Pro	Lys	Asp	Asn	Glu	Asn	Asn	Asn	Glu	Asn	Asn	Asn	Glu	
			230					235					240			
aat	aac	acc	aaa	gag	aat	aca	aag	agc	gag	tcg	tagttgaaag	aatttgattt				889
Asn	Asn	Thr	Lys	Glu	Asn	Thr	Lys	Ser	Glu	Ser						
		245					250									
agaaagctat	gattattatt	tcgctaagga	attgatcgca	agctaccccg	ttttgccc	aa										949
agaaaaggct	aaattactcg	tctatgaaag	gcgttcgcaa													989

<210> 130  
 <211> 253  
 <212> PRT  
 <213> Helicobacter pylori

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Met	Val	Ser	Val	Gly	Thr	Ile	Leu	Val	Ala	Phe	Leu	Gly	Cys	Phe	His	
			20					25					30			
Phe	Trp	Lys	Ser	Ile	Phe	Glu	Phe	Val	Lys	Asn	Ser	Tyr	Lys	Gly	Thr	
		35					40					45				
Leu	Ile	Gln	Leu	Ser	Pro	Ile	Glu	Gly	Val	Met	Val	Ala	Val	Lys	Ile	
	50					55					60					
Ser	Phe	Ser	Ala	Ala	Ile	Val	Ile	Ser	Met	Pro	Ile	Ile	Phe	Trp	Gln	
65					70					75					80	
Leu	Trp	Leu	Phe	Ile	Ala	Pro	Gly	Leu	Tyr	Lys	Asn	Glu	Lys	Lys	Val	
				85					90					95		
Ile	Leu	Pro	Phe	Val	Phe	Phe	Gly	Ser	Gly	Met	Phe	Leu	Ile	Gly	Ala	
			100				105							110		
Ala	Phe	Ser	Tyr	Tyr	Val	Val	Phe	Pro	Phe	Ile	Ile	Glu	Tyr	Leu	Ala	
		115				120						125				
Thr	Phe	Gly	Ser	Asp	Val	Phe	Ala	Ala	Asn	Ile	Ser	Ala	Ser	Ser	Tyr	
	130				135						140					
Val	Ser	Phe	Phe	Thr	Arg	Leu	Ile	Leu	Gly	Phe	Gly	Val	Ala	Phe	Glu	
145					150					155					160	
Leu	Pro	Val	Leu	Ala	Tyr	Phe	Leu	Ala	Lys	Val	Gly	Leu	Ile	Thr	Asp	
				165					170					175		
Ala	Ser	Leu	Lys	Ala	Tyr	Phe	Lys	Tyr	Ala	Ile	Val	Val	Ile	Phe	Ile	
			180					185					190			
Val	Ala	Ala	Ile	Ile	Thr	Pro	Pro	Asp	Val	Val	Ser	Gln	Ile	Phe	Met	
	195					200						205				
Ala	Leu	Pro	Leu	Val	Gly	Leu	Tyr	Gly	Leu	Ser	Ile	Leu	Ile	Ala	Lys	
	210					215					220					
Met	Val	Asn	Pro	Ala	Pro	Lys	Asp	Asn	Glu	Asn	Asn	Asn	Glu	Asn	Asn	
225					230				235						240	
Asn	Glu	Asn	Asn	Thr	Lys	Glu	Asn	Thr	Lys	Ser	Glu	Ser				
				245					250							

<210> 131  
 <211> 655  
 <212> DNA  
 <213> Helicobacter pylori  
  
 <220>



[illegible]

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Thr	Leu	Gln	Ala	Asn	Met	Phe	Thr	Tyr	Gly	Val	Gly	Gly	Asp	Phe	Met		
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Leu	Val	Val	Asn	Thr	Trp	Asp	Ser	Leu	Lys	Asp	Phe	Asn	Phe	His	Asn		
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-147-

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Lys	Leu	Leu	Gln 35	Gly	Ala	Ser	Ile 40	Leu	Gln	Gly	Tyr	Glu 45	Val	Asn	Pro
Lys	Asn 50	Asp	Trp	Ala	Tyr	Ser 55	Arg	Tyr	Tyr	Phe	Phe 60	Ile	Asp	Tyr	Gly
Asn 65	Val	Leu	Phe	Asn 70	Asn	Asp	Ser	Thr	Leu	Gln 75	Ala	Asn	Met	Phe	Thr 80
Tyr	Gly	Val	Gly 85	Gly	Asp	Phe	Met	Val	Ala 90	Tyr	Ala	Lys	Asn 95	Pro	Ile
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Ile	Leu	Asn 115	Asn	Lys	Val	Lys	Asp 120	Leu	Val	Val	Asn	Thr 125	Trp	Asp	Ser
Leu	Lys 130	Asp	Phe	Asn	Phe	His 135	Asn	Thr	Tyr	Phe	Arg 140	Ala	Ile	Gly	Lys
Phe 145	Gly	Val	Gln	Phe 150	Arg	Thr	Ile	Val	Leu	Tyr 155	His	Lys	Val	Asp	Val 160
Glu	Ile	Gly	Met 165	Lys	Ile	Phe	Leu	Thr	Pro 170	Glu	Arg	Arg	Ser	Leu 175	Phe
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<213> Helicobacter pylori

<221> CDS

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-148-

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<210> 134

<212> PRT

<400> 134

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Asn	Phe	Lys	Val	Gln	Asn	Val	Asp	Gly	Lys	Asp	Asn	Leu	Ser	Lys	Arg
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Leu	Leu	Glu	Ile	Glu	Lys	Tyr	Asp	Lys	Thr	Leu	Ile	Ile	Phe	Asp	Ala
	50					55					60				
Asp	Lys	Asp	Tyr	Glu	Ser	Asn	Lys	Lys	Glu	Ile	Leu	Lys	Ile	Val	Ser

Val Phe Leu Glu Val Tyr Leu Tyr Phe Leu Glu Arg Phe Pro Ile Lys

Asn Phe Lys Val Gln Asn Val Asp Gly Lys Asp Asn Leu Ser Lys Arg

Leu Leu Glu Ile Glu Lys Tyr Asp Lys Thr Leu Ile Ile Phe Asp Ala

Asp Lys Asp Tyr Glu Ser Asn Lys Lys Glu Ile Leu Lys Ile Val Ser



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Ile	Val	Leu	Asn	Leu	Val	Asn	Arg	Ala	Leu	Ala	Ala	Pro	Leu	Asn	Ile			
			110				115				120							
cat	ggc	gat	cat	tct	gat	atg	tat	tta	agc	agg	gat	tct	ggg	tgg	ata		494	
His	Gly	Asp	His	Ser	Asp	Met	Tyr	Leu	Ser	Arg	Asp	Ser	Gly	Trp	Ile			
			125				130				135							
agt	tta	tgc	aca	tgc	aac	ccc	caa	gaa	gct	tat	gat	ttc	act	tta	atg		542	
Ser	Leu	Cys	Thr	Cys	Asn	Pro	Gln	Glu	Ala	Tyr	Asp	Phe	Thr	Leu	Met			
			140				145				150				155			
gcg	ttt	aga	atc	gca	gag	cat	caa	aag	gtg	cgc	gtg	cct	act	att	gtc		590	
Ala	Phe	Arg	Ile	Ala	Glu	His	Gln	Lys	Val	Arg	Val	Pro	Thr	Ile	Val			
			160				165				170							
aat	caa	gac	ggg	ttt	tta	tgc	tcg	cac	acc	gtg	caa	aat	gtc	cgc	cct		638	
Asn	Gln	Asp	Gly	Phe	Leu	Cys	Ser	His	Thr	Val	Gln	Asn	Val	Arg	Pro			
			175				180				185							
ttg	agc	gat	gca	gtg	gct	tac	caa	ttc	gtg	ggc	gaa	tac	caa	acc	aag		686	
Leu	Ser	Asp	Ala	Val	Ala	Tyr	Gln	Phe	Val	Gly	Glu	Tyr	Gln	Thr	Lys			
			190				195				200							
cat	tcc	ctt	ttg	gat	ttt	gat	aaa	cgc	gta	agc	tat	ggc	gcg	caa	gct		734	
His	Ser	Leu	Leu	Asp	Phe	Asp	Lys	Pro	Val	Ser	Tyr	Gly	Ala	Gln	Ala			
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gaa	gaa	gaa	tgg	cat	tat	gag	cat	aaa	gcc	caa	ctc	cac	cat	gcc	atc		782	
Glu	Glu	Glu	Trp	His	Tyr	Glu	His	Lys	Ala	Gln	Leu	His	His	Ala	Ile			
			220				225				230				235			
atg	agc	gcg	tct	tct	gtg	att	gaa	gaa	gtg	ttc	aat	gat	ttc	gct	aaa		830	
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ctc	aca	ggc	agg	caa	tac	cat	tta	acc	aaa	act	ttc	cag	cta	gaa	gac		878	
Leu	Thr	Gly	Arg	Gln	Tyr	His	Leu	Thr	Lys	Thr	Phe	Gln	Leu	Glu	Asp			
			255				260				265							
gct	gaa	atc	gct	atc	ttt	gcg	tta	ggc	act	act	tat	gaa	tca	gcg	atc		926	
Ala	Glu	Ile	Ala	Ile	Phe	Ala	Leu	Gly	Thr	Thr	Tyr	Glu	Ser	Ala	Ile			
			270				275				280							
gta	gcg	gct	aaa	gaa	atg	cgt	aaa	aaa	ggc	att	aag	gcc	ggc	gtg	gct		974	
Val	Ala	Ala	Lys	Glu	Met	Arg	Lys	Lys	Gly	Ile	Lys	Ala	Gly	Val	Ala			
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Thr	Ile	His	Ser	Leu	Arg	Pro	Phe	Pro	Tyr	Glu	Arg	Leu	Gly	Gln	Asp			
			300				305				310				315			
ttg	aaa	aat	ctt	aaa	gct	tta	gcg	att	tta	gac	aag	agc	tct	cca	gcg		1070	
Leu																		

Gly	Thr	Met	Gly	Ala	Met	Phe	Asn	Glu	Val	Thr	Ser	Ala	Val	Tyr	Gln		
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Thr	Gln	Gly	Thr	Lys	His	Pro	Val	Val	Ser	Asn	Tyr	Ile	Tyr	Gly	Leu		
		350					355					360					
ggc	gaa	agg	gat	atg	acg	atc	gcg	cat	tta	tgc	gaa	att	ttt	gaa	gaa	1214	
Gly	Glu	Arg	Asp	Met	Thr	Ile	Ala	His	Leu	Cys	Glu	Ile	Phe	Glu	Glu		
		365				370					375						
atc	aat	gaa	gac	gct	ctt	aaa	ggc	acg	ctc	acg	cac	cct	acc	caa	caa	1262	
Ile	Asn	Glu	Asp	Ala	Leu	Lys	Gly	Thr	Leu	Thr	His	Pro	Thr	Gln	Gln		
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Phe	Val	Gly	Leu	His	Gly	Pro	Lys	Met	Ser	Phe	Phe						
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 <213> Helicobacter pylori

<400> 136

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		35					40					45					
Phe	Lys	Asp	Asn	Gly	Tyr	Val	Asp	Gly	Glu	Phe	Val	Leu	Val	Glu	Ser		
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Glu	His	Ala	Ala	Met	Ser	Ala	Cys	Val	Gly	Ala	Ala	Ala	Ala	Gly	Gly		
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Arg	Val	Ser	Thr	Ala	Thr	Ser	Ser	Gln	Gly	Leu	Ala	Leu	Met	Val	Glu		
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Leu	Cys	Ser	His	Thr	Val	Gln	Asn	Val	Arg	Pro	Leu	Ser	Asp	Ala	Val		
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Phe	Asp	Lys	Pro	Val	Ser	Tyr	Gly	Ala	Gln	Ala	Glu	Glu	Glu	Trp	His		
	210					215					220						
Tyr	Glu	His	Lys	Ala	Gln	Leu	His	His	Ala	Ile	Met	Ser	Ala	Ser	Ser		
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      275      280      285
Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala Thr Ile His Ser Leu
      290      295      300
Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp Leu Lys Asn Leu Lys
      305      310      315      320
Ala Leu Ala Ile Leu Asp Lys Ser Ser Pro Ala Gly Thr Met Gly Ala
      325      330      335
Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln Thr Gln Gly Thr Lys
      340      345      350
His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu Gly Glu Arg Asp Met
      355      360      365
Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu Ile Asn Glu Asp Ala
      370      375      380
Leu Lys Gly Thr Leu Thr His Pro Thr Gln Gln Phe Val Gly Leu His
      385      390      395      400
Gly Pro Lys Met Ser Phe Phe
      405

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 <213> Helicobacter pylori

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 <222> (1)...(855)

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Lys Ile Glu Val Leu Arg Gly Phe Leu Lys Arg Ala Leu Tyr Leu Ile
  1              5              10              15

tta ggg ctt ttt tac acg ctt aat gca gag agc ttt aaa gat gtt ttg      96
Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu
      20              25              30

act aaa gtg gat tac act ttt ttt aat aaa aag gtg gtt tcg ccc atc      144
Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile
      35              40              45

aaa cgc tat gcg gat aga tcg gcg ttt tat ctg ggg ctt ggg tat caa      192
Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln
      50              55              60

tta ggg agc att cag cac aac tct agc aac ttg aat tta tcc cag caa      240
Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln
      65              70              75              80

ttc aat aag agt cag att att ttc agc gat agt cta agc cct gtt ttt      288
Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe
      85              90              95

aaa aat tcg tat gtg tct aat ggc ctt ggc gtg caa gtg ggc tat aag      336
Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys
      100              105              110

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[illegible]

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<212> PRT
<213> Helicobacter pylori
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			20					25					30		
Thr	Lys	Val	Asp	Tyr	Thr	Phe	Phe	Asn	Lys	Lys	Val	Val	Ser	Pro	Ile
		35					40					45			



Lys	Arg	Tyr	Ala	Asp	Arg	Ser	Ala	Phe	Tyr	Leu	Gly	Leu	Gly	Tyr	Gln
50						55					60				
Leu	Gly	Ser	Ile	Gln	His	Asn	Ser	Ser	Asn	Leu	Asn	Leu	Ser	Gln	Gln
65					70				75						80
Phe	Asn	Lys	Ser	Gln	Ile	Ile	Phe	Ser	Asp	Ser	Leu	Ser	Pro	Val	Phe
				85					90					95	
Lys	Asn	Ser	Tyr	Val	Ser	Asn	Gly	Leu	Gly	Val	Gln	Val	Gly	Tyr	Lys
				100				105					110		
Trp	Val	Gly	Lys	His	Glu	Glu	Thr	Lys	Trp	Phe	Gly	Phe	Arg	Trp	Gly
		115					120					125			
Leu	Phe	Tyr	Asp	Leu	Ser	Ala	Ser	Leu	Tyr	Gly	Gln	Lys	Glu	Ser	Gln
		130				135					140				
Ser	Val	Ile	Ile	Ser	Thr	Tyr	Gly	Thr	Tyr	Met	Asp	Leu	Leu	Leu	Asn
145					150					155					160
Ala	Tyr	Asn	Gly	Asp	Lys	Phe	Phe	Ala	Gly	Phe	Asn	Leu	Gly	Ile	Ala
				165					170					175	
Phe	Ala	Gly	Val	Tyr	Asp	Lys	Val	Ser	Asp	Ala	Leu	Leu	Tyr	Gln	Ala
				180				185					190		
Leu	Leu	Leu	Asp	Thr	Phe	Gly	Gly	Lys	Val	Asp	Pro	Asn	Gly	Phe	Gln
		195					200					205			
Phe	Leu	Val	Asn	Leu	Gly	Val	Arg	Leu	Gly	Asn	Lys	His	Asn	Gln	Phe
		210				215					220				
Gly	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Tyr	Tyr	Phe	Asn	His	Tyr	Tyr	Ser
225					230					235					240
Met	Asn	Asn	Ile	Ser	Asn	Asn	Ser	Glu	Asp	Val	Leu	Lys	Val	Leu	Arg
				245					250					255	
Phe	Leu	Glu	Tyr	Gly	Ile	Asn	Ser	Leu	Leu	Tyr	Gln	Val	Asp	Phe	Arg
			260					265					270		
Arg	Asn	Tyr	Ser	Val	Tyr	Phe	Asn	Tyr	Thr	Tyr	Ile	Phe			
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 <213> Helicobacter pylori

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				1						5						
acg	att	ggc	ttg	ggt	gtg	ata	gca	ctc	ttt	ttg	ggt	ttg	tta	aac	cct	103
Thr	Ile	Gly	Leu	Gly	Val	Ile	Ala	Leu	Phe	Leu	Gly	Leu	Leu	Asn	Pro	
		10					15					20				
ttg	agt	gcg	gcg	agt	tac	ccc	ccc	att	aaa	aac	act	aaa	gta	ggc	tta	151
Leu	Ser	Ala	Ala	Ser	Tyr	Pro	Pro	Ile	Lys	Asn	Thr	Lys	Val	Gly	Leu	
		25					30				35					
gcc	ctt	tct	agc	cac	ccg	cta	gct	agt	gag	atc	ggg	caa	aag	gtt	tta	199
Ala	Leu	Ser	Ser	His	Pro	Leu	Ala	Ser	Glu	Ile	Gly	Gln	Lys	Val	Leu	
		40				45				50					55	
gaa	gag	gga	ggt	aat	gcg	att	gat	gcg	gct	gta	gcg	ata	ggt	ttt	gct	247
Glu	Glu	Gly	Gly	Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Ile	Gly	Phe	Ala	

				60				65				70							
ctt	gcg	gtt	gtc	cat	ccg	gca	gca	ggc	aat	att	ggt	gga	ggc	ggt	ttt	295			
Leu	Ala	Val	Val	His	Pro	Ala	Ala	Gly	Asn	Ile	Gly	Gly	Gly	Gly	Phe				
75								80				85							
gcg	gtt	atc	cat	ttg	gct	aat	ggt	gaa	aat	gtt	gcg	tta	gat	ttt	aga	343			
Ala	Val	Ile	His	Leu	Ala	Asn	Gly	Glu	Asn	Val	Ala	Leu	Asp	Phe	Arg				
90								95				100							
gaa	aaa	gcc	ccc	tta	aaa	gcc	act	aaa	aac	atg	ttt	tta	gac	aag	caa	391			
Glu	Lys	Ala	Pro	Leu	Lys	Ala	Thr	Lys	Asn	Met	Phe	Leu	Asp	Lys	Gln				
105								110				115							
ggc	aat	gta	gtc	cct	aaa	ctc	agc	gaa	gat	ggc	tat	ttg	gcg	gcc	ggg	439			
Gly	Asn	Val	Val	Pro	Lys	Leu	Ser	Glu	Asp	Gly	Tyr	Leu	Ala	Ala	Gly				
120				125				130				135							
gtt	cct	gga	acg	gtg	gca	ggc	atg	gaa	gcg	atg	ctg	aaa	aaa	tac	ggc	487			
Val	Pro	Gly	Thr	Val	Ala	Gly	Met	Glu	Ala	Met	Leu	Lys	Lys	Tyr	Gly				
				140				145				150							
act	aaa	aaa	cta	tcg	caa	ctc	att	gat	cct	gcc	att	aaa	ttg	gct	gaa	535			
Thr	Lys	Lys	Leu	Ser	Gln	Leu	Ile	Asp	Pro	Ala	Ile	Lys	Leu	Ala	Glu				
				155				160				165							
aat	ggt	tat	gcg	att	tca	caa	aga	caa	gca	gaa	acc	cta	aag	gaa	gca	583			
Asn	Gly	Tyr	Ala	Ile	Ser	Gln	Arg	Gln	Ala	Glu	Thr	Leu	Lys	Glu	Ala				
				170				175				180							
agg	gag	cgg	ttt	tta	aaa	tac	agt	tct	agc	aaa	aag	tat	ttt	ttt	aaa	631			
Arg	Glu	Arg	Phe	Leu	Lys	Tyr	Ser	Ser	Ser	Lys	Lys	Tyr	Phe	Phe	Lys				
				185				190				195							
aaa	ggc	cat	ctt	gat	tat	caa	gaa	ggg	gat	ttg	ttt	gtc	caa	aaa	gat	679			
Lys	Gly	His	Leu	Asp	Tyr	Gln	Glu	Gly	Asp	Leu	Phe	Val	Gln	Lys	Asp				
200				205				210				215							
tta	gcc	aag	act	ttg	aat	caa	atc	aaa	acg	cta	ggc	gct	aaa	ggc	ttt	727			
Leu	Ala	Lys	Thr	Leu	Asn	Gln	Ile	Lys	Thr	Leu	Gly	Ala	Lys	Gly	Phe				
				220				225				230							
tat	caa	ggg	caa	gtc	gct	gag	ctt	att	gag	aaa	gac	atg	aaa	aaa	aat	775			
Tyr	Gln	Gly	Gln	Val	Ala	Glu	Leu	Ile	Glu	Lys	Asp	Met	Lys	Lys	Asn				
				235				240				245							
gga	ggg	att	atc	act	aaa	gaa	gat	tta	gcc	agt	tac	aat	gtg	aaa	tgg	823			
Gly	Gly	Ile	Ile	Thr	Lys	Glu	Asp	Leu	Ala	Ser	Tyr	Asn	Val	Lys	Trp				
				250				255				260							
cgc	aaa	ccc	gtg	gta	ggg	agt	tat	cgt	ggg	tat	aag	atc	att	tct	atg	871			
Arg	Lys	Pro	Val	Val	Gly	Ser	Tyr	Arg	Gly	Tyr	Lys	Ile	Ile	Ser	Met				
				265				270				275							
tcg	ccg	cca	agt	tcg	gga	ggc	acg	cat	ttg	atc	cag	att	tta	aat	gtc	919			
Ser	Pro	Pro	Ser	Ser	Gly	Gly	Thr	His	Leu	Ile	Gln	Ile	Leu	Asn	Val				
280				285				290				295							
atg	gaa	aat	gcg	gat	tta	agc	gcc	ctt	ggg	tat	ggg	gct	tct	aag	aat	967			



act aag ccg gtc atg ggt gat gtg aat gcg atc caa gtt ttg cct aaa 1687  
 Thr Lys Pro Val Met Gly Asp Val Asn Ala Ile Gln Val Leu Pro Lys  
                   540                  545                  550

act aaa ggg agc gtt ttc tat ggt tca acg gat cca agg aaa gaa ttt 1735  
 Thr Lys Gly Ser Val Phe Tyr Gly Ser Thr Asp Pro Arg Lys Glu Phe  
                   555                  560                  565

taattcttttg tcatatacag gtttttaatc ctatttagcc ttatttttttg ggatggaggg 1795  
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           20                  25                  30  
 Lys Asn Thr Lys Val Gly Leu Ala Leu Ser Ser His Pro Leu Ala Ser  
           35                  40                  45  
 Glu Ile Gly Gln Lys Val Leu Glu Glu Gly Gly Asn Ala Ile Asp Ala  
   50                  55                  60  
 Ala Val Ala Ile Gly Phe Ala Leu Ala Val Val His Pro Ala Ala Gly  
   65                  70                  75                  80  
 Asn Ile Gly Gly Gly Gly Phe Ala Val Ile His Leu Ala Asn Gly Glu  
           85                  90                  95  
 Asn Val Ala Leu Asp Phe Arg Glu Lys Ala Pro Leu Lys Ala Thr Lys  
           100                  105                  110  
 Asn Met Phe Leu Asp Lys Gln Gly Asn Val Val Pro Lys Leu Ser Glu  
           115                  120                  125  
 Asp Gly Tyr Leu Ala Ala Gly Val Pro Gly Thr Val Ala Gly Met Glu  
   130                  135                  140  
 Ala Met Leu Lys Lys Tyr Gly Thr Lys Lys Leu Ser Gln Leu Ile Asp  
   145                  150                  155                  160  
 Pro Ala Ile Lys Leu Ala Glu Asn Gly Tyr Ala Ile Ser Gln Arg Gln  
           165                  170                  175  
 Ala Glu Thr Leu Lys Glu Ala Arg Glu Arg Phe Leu Lys Tyr Ser Ser  
           180                  185                  190  
 Ser Lys Lys Tyr Phe Phe Lys Lys Gly His Leu Asp Tyr Gln Glu Gly  
           195                  200                  205  
 Asp Leu Phe Val Gln Lys Asp Leu Ala Lys Thr Leu Asn Gln Ile Lys  
   210                  215                  220  
 Thr Leu Gly Ala Lys Gly Phe Tyr Gln Gly Gln Val Ala Glu Leu Ile  
   225                  230                  235                  240  
 Glu Lys Asp Met Lys Lys Asn Gly Gly Ile Ile Thr Lys Glu Asp Leu  
           245                  250                  255  
 Ala Ser Tyr Asn Val Lys Trp Arg Lys Pro Val Val Gly Ser Tyr Arg  
           260                  265                  270  
 Gly Tyr Lys Ile Ile Ser Met Ser Pro Pro Ser Ser Gly Gly Thr His  
           275                  280                  285  
 Leu Ile Gln Ile Leu Asn Val Met Glu Asn Ala Asp Leu Ser Ala Leu  
   290                  295                  300  
 Gly Tyr Gly Ala Ser Lys Asn Ile His Ile Ala Ala Glu Ala Met Arg  
   305                  310                  315                  320  
 Gln Ala Tyr Ala Asp Arg Ser Val Tyr Met Gly Asp Ala Asp Phe Val  
           325                  330                  335

Ser Val Pro Val Asp Lys Leu Ile Asn Lys Ala Tyr Ala Lys Lys Ile  
 340 345 350  
 Phe Asp Thr Ile Gln Pro Asp Thr Val Thr Pro Ser Ser Gln Ile Lys  
 355 360 365  
 Pro Gly Met Gly Gln Leu His Glu Gly Ser Asn Thr Thr His Tyr Ser  
 370 375 380  
 Val Ala Asp Arg Trp Gly Asn Ala Val Ser Val Thr Tyr Thr Ile Asn  
 385 390 395 400  
 Ala Ser Tyr Gly Ser Ala Ala Ser Ile Asp Gly Ala Gly Phe Leu Leu  
 405 410 415  
 Asn Asn Glu Met Asp Asp Phe Ser Ile Lys Pro Gly Asn Pro Asn Leu  
 420 425 430  
 Tyr Gly Leu Val Gly Gly Asp Ala Asn Ala Ile Glu Ala Asn Lys Arg  
 435 440 445  
 Pro Leu Ser Ser Met Ser Pro Thr Ile Val Leu Lys Asn Asn Lys Val  
 450 455 460  
 Phe Leu Val Val Gly Ser Pro Gly Gly Ser Arg Ile Ile Thr Thr Val  
 465 470 475 480  
 Leu Gln Val Ile Ser Asn Val Ile Asp Tyr Asn Met Asn Ile Ser Glu  
 485 490 495  
 Ala Val Ser Ala Pro Arg Phe His Met Gln Trp Leu Pro Asp Glu Leu  
 500 505 510  
 Arg Ile Glu Lys Phe Gly Met Pro Ala Asp Val Lys Asp Asn Leu Thr  
 515 520 525  
 Lys Met Gly Tyr Gln Ile Val Thr Lys Pro Val Met Gly Asp Val Asn  
 530 535 540  
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 Thr Asp Pro Arg Lys Glu Phe  
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 Met Gln Asn His Asp Leu Glu Ser Ile Lys Gln Ala  
 1 5 10  
 gct ttg att gaa tat gaa gtg aga gaa caa ggc tct agt att gtg cta 159  
 Ala Leu Ile Glu Tyr Glu Val Arg Glu Gln Gly Ser Ser Ile Val Leu  
 15 20 25  
 gac agc aat att tcc aaa gag cct tta gag ttt att ata ggc act aat 207  
 Asp Ser Asn Ile Ser Lys Glu Pro Leu Glu Phe Ile Ile Gly Thr Asn  
 30 35 40  
 caa atc ata gca ggg tta gaa aag gcg gta tta aag gct caa att ggc 255  
 Gln Ile Ile Ala Gly Leu Glu Lys Ala Val Leu Lys Ala Gln Ile Gly  
 45 50 55 60  
 gag tgg gaa gag gtt gtc atc gcc cca gag gaa gct tat ggg gtt tat 303





50 55 60  
 Leu Thr Thr Asn Ile His Gln Leu Pro Lys Pro Ile Ala Thr Arg Leu  
 65 70 75 80  
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 Ser Ala Cys Phe Ser Phe Cys Asn Cys Phe Ala Asn Ala Ser Asn Ser  
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 Glu His Asn Thr Asn Ile Ala Thr Glu Phe Arg Ala Gly Leu Thr Thr  
 10 15 20  
 ttt atc acc atg att tac atc gtg ccc tta aac gct ctt atc ctt tct 150  
 Phe Ile Thr Met Ile Tyr Ile Val Pro Leu Asn Ala Leu Ile Leu Ser  
 25 30 35  
 caa gcc aac atg cct tat gaa gcc ctt tta agt gca acg gcc att atc 198  
 Gln Ala Asn Met Pro Tyr Glu Ala Leu Leu Ser Ala Thr Ala Ile Ile  
 40 45 50 55  
 act atc tta tcg agc gtg ttt aac gga ttg tgg gca aac acc cct atc 246  
 Thr Ile Leu Ser Ser Val Phe Asn Gly Leu Trp Ala Asn Thr Pro Ile  
 60 65 70  
 gct atg agc gtg ggc tta ggg ctg tca gct tat ttt agc ttc ggg ttg 294  
 Ala Met Ser Val Gly Leu Gly Leu Ser Ala Tyr Phe Ser Phe Gly Leu  
 75 80 85  
 gtt caa ggg tta aaa ctc cct tgg cag agc gct tta ggc atc gta gcg 342  
 Val Gln Gly Leu Lys Leu Pro Trp Gln Ser Ala Leu Gly Ile Val Ala  
 90 95 100  
 ctc tcg gga gcg att ttt gtg att ttg tct ttc act aaa ttt aga agt 390  
 Leu Ser Gly Ala Ile Phe Val Ile Leu Ser Phe Thr Lys Phe Arg Ser  
 105 110 115  
 tgg gtc atg cga agc att cct agc gat tta agg cgt gcg gtg agt gcg 438  
 Trp Val Met Arg Ser Ile Pro Ser Asp Leu Arg Arg Ala Val Ser Ala  
 120 125 130 135  
 ggg ata ggg gct ttt atc gcg ttt att ggc ctt aaa gaa atg cat atc 486  
 Gly Ile Gly Ala Phe Ile Ala Phe Ile Gly Leu Lys Glu Met His Ile  
 140 145 150  
 gtc gtt acc cat aar gct acg ctt gta acc tta ggc gat ttt ggc gat 534









Asp Ser Lys Thr Asn Arg Val Arg Phe Leu Asn His Asp Leu Ser Ala	
115 120 125	
acg cct gat ttt gaa ttg agt tta aga gcg tat caa aca gca aag cgt	494
Thr Pro Asp Phe Glu Leu Ser Leu Arg Ala Tyr Gln Thr Ala Lys Arg	
130 135 140	
ttg ggt att gat ttg aaa gtg ggc aat gtt ttt tca agc gat ttt ttc	542
Leu Gly Ile Asp Leu Lys Val Gly Asn Val Phe Ser Ser Asp Phe Phe	
145 150 155	
tat tct ttt gaa acg cat gcc ttt gat tta atg gct aaa tac aac cac	590
Tyr Ser Phe Glu Thr His Ala Phe Asp Leu Met Ala Lys Tyr Asn His	
160 165 170 175	
ttg gct att gaa atg gaa gcg gcg ggg tta tac gcc acg gcg atg gaa	638
Leu Ala Ile Glu Met Glu Ala Ala Gly Leu Tyr Ala Thr Ala Met Glu	
180 185 190	
cta aac gct aag gct tta tgc tta tgc tca gtc tca gat cac tta atc	686
Leu Asn Ala Lys Ala Leu Cys Leu Cys Ser Val Ser Asp His Leu Ile	
195 200 205	
act aaa gaa gcc tta agc cct aaa gaa agg gta gaa agc ttt gat aac	734
Thr Lys Glu Ala Leu Ser Pro Lys Glu Arg Val Glu Ser Phe Asp Asn	
210 215 220	
atg ata att ttg gct ttg gag atg atg agt tagccttttt tgcccccata	784
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225 230	
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Leu Gln Asp Ala Lys Glu Ile Thr Asn Val Arg Asn Met Leu Gly Phe	
35 40 45	
Ser Gly Lys Tyr Lys Gly Arg Gly Ile Ser Leu Met Gly His Gly Met	
50 55 60	
Gly Ile Ala Ser Cys Thr Ile Tyr Val Thr Glu Leu Ile Lys Thr Tyr	
65 70 75 80	
Gln Val Lys Glu Leu Leu Arg Ile Gly Thr Cys Gly Ala Ile Ser Pro	
85 90 95	
Lys Val Gly Leu Lys Asp Ile Ile Met Ala Thr Gly Ala Ser Thr Asp	
100 105 110	
Ser Lys Thr Asn Arg Val Arg Phe Leu Asn His Asp Leu Ser Ala Thr	
115 120 125	
Pro Asp Phe Glu Leu Ser Leu Arg Ala Tyr Gln Thr Ala Lys Arg Leu	
130 135 140	
Gly Ile Asp Leu Lys Val Gly Asn Val Phe Ser Ser Asp Phe Phe Tyr	
145 150 155 160	





ctc aac aac cct tcc aag caa aaa aat gtc tat ttc ccc tta gac gct 1263  
 Leu Asn Asn Pro Ser Lys Gln Lys Asn Val Tyr Phe Pro Leu Asp Ala  
 380 385 390 395

tac aat gag gaa caa ttt gaa act tta gag gat aaa atc att gaa tgg 1311  
 Tyr Asn Glu Glu Gln Phe Glu Thr Leu Glu Asp Lys Ile Ile Glu Trp  
 400 405 410

tat gtt aat att agc gaa gaa atc att att gtg aaa tat aat tcc gat 1359  
 Tyr Val Asn Ile Ser Glu Glu Ile Ile Ile Val Lys Tyr Asn Ser Asp  
 415 420 425

cac att agc gaa gaa gaa atc att cac tta gcg caa aac ttt aga aaa 1407  
 His Ile Ser Glu Glu Glu Ile Ile His Leu Ala Gln Asn Phe Arg Lys  
 430 435 440

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 Phe His Ser Ser Ser Pro Leu Leu Val Gly Leu Ala Val Gly Gly Ala  
 35 40 45  
 Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met Gly Ile Leu Ser Asp  
 50 55 60  
 Lys Ile Gly Arg Lys Val Val Val Met Val Cys Leu Leu Leu Phe Leu  
 65 70 75 80  
 Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp Ile Val Trp Leu Val  
 85 90 95  
 Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu Gly Gly Val Ile Ser  
 100 105 110  
 Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu Arg Thr Lys Ala Met  
 115 120 125  
 Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe Thr Ile Ser Met Ala  
 130 135 140  
 Ile Gly Pro Gly Val Val Ala Phe Leu Gly Gly Ala Lys Trp Leu Phe  
 145 150 155 160  
 Leu Leu Thr Ala Ile Leu Thr Leu Leu Ser Leu Leu Met Leu Leu Lys  
 165 170 175  
 Val Lys Asp Ala Pro Lys Ile Ser Tyr Gln Ile Lys Asn Ile Lys Ala  
 180 185 190  
 Tyr Gln Pro Asn Ser Lys Ala Leu Tyr Leu Leu Tyr Leu Ser Ser Phe  
 195 200 205  
 Phe Glu Lys Ala Phe Met Thr Leu Ile Phe Val Leu Ile Pro Leu Ala  
 210 215 220  
 Leu Val Asn Glu Phe His Lys Asp Glu Ser Phe Leu Ile Leu Val Tyr  
 225 230 235 240  
 Val Pro Gly Ala Leu Leu Gly Val Leu Ser Met Gly Ile Ala Ser Val  
 245 250 255  
 Met Ala Glu Lys Tyr Asn Lys Pro Lys Gly Val Met Leu Ser Gly Val  
 260 265 270  
 Leu Leu Phe Ile Val Ser Tyr Leu Cys Leu Phe Leu Ala Asp Ser Ser

	275						280					285					
Phe	Leu	Gly	Lys	Tyr	Leu	Trp	Leu	Phe	Ile	Val	Gly	Val	Ala	Phe	Phe		
	290					295					300						
Phe	Ile	Gly	Phe	Ala	Thr	Leu	Glu	Pro	Ile	Met	Gln	Ser	Leu	Ala	Ser		
305					310					315					320		
Lys	Phe	Ala	Lys	Val	His	Glu	Lys	Gly	Lys	Val	Leu	Gly	Gln	Phe	Thr		
					325					330							
Thr	Phe	Gly	Tyr	Leu	Gly	Ser	Phe	Val	Gly	Gly	Val	Ser	Gly	Gly	Leu		
					340					345				350			
Ser	Tyr	His	His	Leu	Gly	Val	Ser	Asn	Thr	Ser	Leu	Ile	Val	Val	Ala		
					355			360					365				
Leu	Gly	Leu	Ile	Trp	Gly	Leu	Ser	Leu	Phe	Leu	Leu	Asn	Asn	Pro	Ser		
	370					375					380						
Lys	Gln	Lys	Asn	Val	Tyr	Phe	Pro	Leu	Asp	Ala	Tyr	Asn	Glu	Glu	Gln		
385					390					395					400		
Phe	Glu	Thr	Leu	Glu	Asp	Lys	Ile	Ile	Glu	Trp	Tyr	Val	Asn	Ile	Ser		
					405					410							
Glu	Glu	Ile	Ile	Ile	Val	Lys	Tyr	Asn	Ser	Asp	His	Ile	Ser	Glu	Glu		
					420				425				430				
Glu	Ile	Ile	His	Leu	Ala	Gln	Asn	Phe	Arg	Lys							
		435					440										

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<220>
<221> CDS
<222> (89)...(1237)
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-170-





Phe Ala Leu Gly Ala Ser Met Pro Leu Thr Phe Leu Val Thr Thr Ala  
 330 335 340

gca gta ggc tta aaa gcg caa gcg atc tca caa aac acc tac tac gca 1168  
 Ala Val Gly Leu Lys Ala Gln Ala Ile Ser Gln Asn Thr Tyr Tyr Ala  
 345 350 355 360

ttg ctc atg gcg gct att ttt gaa ggg gta tta ttc acg att gcg atc 1216  
 Leu Leu Met Ala Ala Ile Phe Glu Gly Val Leu Phe Thr Ile Ala Ile  
 365 370 375

aaa ata ctc aac aaa aaa gct tgaatgaaag ctttaagcgct taaatattta 1267  
 Lys Ile Leu Asn Lys Lys Ala  
 380

gcgtcgctaa agctgttcgc ttgaacatta ttgaacgcat tctctaagct atcaaagaaa 1327  
 cgagggtgca agttttgcat ttcttttaag aaa 1360

<210> 152  
 <211> 383  
 <212> PRT  
 <213> Helicobacter pylori

<400> 152

Met His Ala Glu Phe Phe Thr Phe Ala Leu Ile Met Leu Leu Ile Val  
 1 5 10 15

Met Ala Pro Tyr Met Ser Arg Ile Ser Arg Leu Pro Ile Thr Val Val  
 20 25 30

Glu Ile Leu Phe Gly Ser Val Gly Ala Tyr Val Gly Phe Ile Glu Pro  
 35 40 45

Thr Lys Gly Phe Glu Ile Met Ser Glu Ile Gly Phe Leu Phe Leu Met  
 50 55 60

Phe Leu Cys Gly Leu Glu Val Glu Ile Tyr Leu Phe Lys Lys Leu Gly  
 65 70 75 80

Val Ser Leu Leu Lys Arg Ile Phe Ala Tyr Leu Leu Ile Leu Tyr Thr  
 85 90 95

Leu Ser Phe Ile Leu Thr Phe Ser Leu Asn Leu Glu Pro Ile Phe Met  
 100 105 110

Val Ile Phe Pro Ile Ile Ser Leu Gly Met Ile Met Thr Leu Val Lys  
 115 120 125

Asp Tyr Arg Lys Glu Ile Leu Trp Leu Asp Leu Val Leu Lys Val Gly  
 130 135 140

Val Ile Gly Glu Leu Leu Ser Ile Phe Gly Leu Val Val Val Asp Gly  
 145 150 155 160

Val Tyr Ser His Gly Leu Gly Met Asp Leu Ile Lys Asp Leu Gly Ile  
 165 170 175

Leu Ile Val Phe Leu Ile Leu Ile Ile Val Ala Phe Gln Ile Phe Lys  
 180 185 190

Thr Leu Phe Trp Trp Phe Pro His Leu Lys Leu Phe Val Met Pro Lys  
 195 200 205

Ser Ser Gln Phe Asn Gln Asp Val Arg Phe Ser Leu Met Leu Phe Phe  
 210 215 220

Ser Leu Val Ala Ile Val Val Trp Leu Lys Ile Glu Met Val Leu Gly  
 225 230 235 240

Ala Phe Leu Ala Gly Leu Val Val Ser Thr Phe Phe Pro His Lys Ser  
 245 250 255

Glu Leu Ile His Lys Leu Asn Asp Val Gly Phe Gly Phe Phe Val Pro  
 260 265 270

Leu Phe Phe Ile His Val Gly Ser Thr Leu Asp Leu Lys Leu Val Phe

275	280	285
Leu Asn Pro His Leu Ile	Leu Gln Gly Ile Leu Ile	Val Ile Ala Met
290	295	300
Leu Ser Leu His Leu Ile	Thr Ser Thr Leu Leu	Trp Arg Lys Tyr Phe
305	310	315
Lys Glu Ala Lys His Leu Phe	Ser Phe Ala Leu Gly	Ala Ser Met Pro
325	330	335
Leu Thr Phe Leu Val Thr Thr	Ala Ala Val Gly Leu Lys	Ala Gln Ala
340	345	350
Ile Ser Gln Asn Thr Tyr Tyr	Ala Leu Leu Met Ala Ala	Ile Phe Glu
355	360	365
Gly Val Leu Phe Thr Ile Ala	Ile Lys Ile Leu Asn Lys	Lys Ala
370	375	380

<210> 153  
 <211> 1024  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (115)...(921)

<400> 153	
agttggcaaa aacgcagaga cagtaacgca aaggcaaata aagagactca ttttaaacaa	60
gcgaatgccca ttacaaatat aatcagatca gttggtgggt tttttacaaa gatt atg	117
	Met
	1
aag aga gtt aga gaa ctt gta aaa aaa cat ccc gag aaa agc agt gtg	165
Lys Arg Val Arg Glu Leu Val Lys Lys His Pro Glu Lys Ser Ser Val	
	5 10 15
gca tta gta gta tta acc cat gct gca tgc aag aaa gcg aaa gaa ttg	213
Ala Leu Val Val Leu Thr His Ala Ala Cys Lys Lys Ala Lys Glu Leu	
	20 25 30
gac gat aaa gtc cag gat aaa tcc aaa caa gct gaa aaa gaa aat caa	261
Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu Asn Gln	
	35 40 45
atc aat tgg tgg aaa tat tca gga tta aca ata gcg aca agt tta tta	309
Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser Leu Leu	
	50 55 60 65
tta gcc gct tgt agt gtt ggt gat att gat aaa cag ata gag tta gaa	357
Leu Ala Ala Cys Ser Val Gly Asp Ile Asp Lys Gln Ile Glu Leu Glu	
	70 75 80
caa gaa aaa aag gaa gct gaa aac gct agg gat aga gcg aac aag agt	405
Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn Lys Ser	
	85 90 95
ggg ata gaa ctg gaa cag gaa aaa caa aag acc att aaa gaa caa aaa	453
Gly Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ile Lys Glu Gln Lys	
	100 105 110
gat tta gtt aaa aaa gca gaa caa aat tgc caa gaa aat cat ggc caa	501
Asp Leu Val Lys Lys Ala Glu Gln Asn Cys Gln Glu Asn His Gly Gln	



Ser Gly Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ile Lys Glu Gln  
 100 105 110  
 Lys Asp Leu Val Lys Lys Ala Glu Gln Asn Cys Gln Glu Asn His Gly  
 115 120 125  
 Gln Phe Phe Met Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala Ile Glu  
 130 135 140  
 Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn Gln Thr  
 145 150 155 160  
 Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His Ser Gln  
 165 170 175  
 Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu  
 180 185 190  
 Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asn Phe  
 195 200 205  
 Tyr Arg Pro Ser Ser Val Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe  
 210 215 220  
 Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys  
 225 230 235 240  
 Ala Gln Ala Lys Met Leu Gly Asn Glu Lys Pro Thr Ser Pro Pro Phe  
 245 250 255  
 Asn Leu Ser Lys Pro Phe Val Arg Ser Lys Asn Ile Cys  
 260 265

<210> 155  
 <211> 535  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(482)

<400> 155  
 gtgatcccta aagaatatat cctgcggtgg ataagggtat ccaagaagcg atg caa 56  
 Met Gln  
 1  
 aat ggc gtt ttg gca ggc tat ccg gtg gtg gat ttt aaa gtt acc ctt 104  
 Asn Gly Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val Thr Leu  
 5 10 15  
 tat gat ggg agc tac cat gat gtg gat tct tca gaa atg gcg ttt aaa 152  
 Tyr Asp Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys  
 20 25 30  
 atc gct ggc tct atg gcg ttt aaa gaa gcg agt cgc gcg gct aac ccg 200  
 Ile Ala Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro  
 35 40 45 50  
 gtt tta cta gag cct atg atg aaa gtg gaa gtg gaa gtc cct gaa gaa 248  
 Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu  
 55 60 65  
 tac atg ggc gat gtg att ggc gat ttg aat aga aga aga ggg caa atc 296  
 Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile  
 70 75 80  
 aat tct atg gac gat aga tta ggc ttg aaa atc gtg aac gct ttt gtg 344  
 Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val

85	90	95	
ccg ttg gtg gaa atg ttt ggc tat tct acg gat tta cga tca gcc acc			392
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr			
100	105	110	
caa ggg cgt ggg act tac tct atg gag ttt gat cat tat ggc gaa gtg			440
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val			
115	120	125 130	
cct agc aat atc gct aag gaa att gta gaa aag cgc aaa ggc			482
Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly			
135	140		
tgatttaatt ataacgctct cttattttta gggggtgta taggtgctgt tta			535

<210> 156  
 <211> 144  
 <212> PRT  
 <213> Helicobacter pylori

<400> 156

Met Gln Asn Gly Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val	
1 5 10 15	
Thr Leu Tyr Asp Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala	
20 25 30	
Phe Lys Ile Ala Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala	
35 40 45	
Asn Pro Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro	
50 55 60	
Glu Glu Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly	
65 70 75 80	
Gln Ile Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala	
85 90 95	
Phe Val Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser	
100 105 110	
Ala Thr Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly	
115 120 125	
Glu Val Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly	
130 135 140	

<210> 157  
 <211> 740  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(671)

<400> 157	
ctctctcttc aagcttggat aacaaatgcg gtttgaagag ttctaacgcc atg ttt	56
	Met Phe
	1
tta ggc aac ccg cat tca tcc att ttg aga tta ggc cca acc aca atc	104
Leu Gly Asn Pro His Ser Ser Ile Leu Arg Leu Gly Pro Thr Thr Ile	
5 10 15	













Lys Ile Thr Thr His Gln Arg Ala Thr Phe Asp Phe Lys Thr Leu Asp  
165 170 175  
Tyr Lys Pro Phe Asp Glu Lys Thr Ser His Lys Ile Ile Ala Val Leu  
180 185 190  
Asp Phe Gly Ala Lys Gly Asn Ile Leu Asn Glu Leu Gln Asn Val Gly  
195 200 205  
Leu Lys Ala Leu Ile Tyr Pro His His Thr Lys Ala Ser Glu Leu Ile  
210 215 220  
Lys Ala Tyr Glu Lys Lys Glu Ile Ser Gly Ile Phe Leu Ser Asn Gly  
225 230 235 240  
Pro Gly Asp Pro Leu Ser Leu Gln Gln Glu Ile Gly Glu Ile Lys Gln  
245 250 255  
Leu Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln  
260 265 270  
Leu Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly  
275 280 285  
His His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val  
290 295 300  
Glu Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu  
305 310 315 320  
Glu Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu  
325 330 335  
Gly Val Arg Tyr Lys Asn Ala Pro Ile Ile Ser Val Gln His His Pro  
340 345 350  
Glu Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe  
355 360 365  
Val Glu Leu Leu Lys Asp Phe  
370 375

<210> 163  
<211> 2790  
<212> DNA  
<213> Helicobacter pylori  
  
<220>  
<221> CDS  
<222> (116)...(2656)

<400> 163  
ttctccttta attttgatg tttaaagtat aataaactat cttttttaaaa aaataactta 60  
aaagagctat aaaatagcct taaaatacgc gataaaacaa caaaaaggaa taccc atg 118  
Met  
1  
  
gat att cgc aac gaa ttt tta caa ttt ttt caa aat aaa ggg cat gcc 166  
Asp Ile Arg Asn Glu Phe Leu Gln Phe Phe Gln Asn Lys Gly His Ala  
5 10 15  
  
gtt tat cct agc atg cct tta gtg cct aat gac gct acc ttg ctt ttt 214  
Val Tyr Pro Ser Met Pro Leu Val Pro Asn Asp Ala Thr Leu Leu Phe  
20 25 30  
  
acc aat gcc ggc atg gtg caa ttt aaa gat att ttt acc ggg att gtg 262  
Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile Val  
35 40 45  
  
cca cgc cct agc att cct aga gcg gca agc tcg caa ttg tgc atg cgc 310  
Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met Arg  
50 55 60 65







cat gaa aga ttg ctc gct atg gtg ttt aaa aaa gaa aat gag cga atc	2470
His Glu Arg Leu Leu Ala Met Val Phe Lys Lys Glu Asn Glu Arg Ile	
770 775 780 785	
act ctc gca tgc ggg gtg aaa aac gcg ccc ata aaa gcg aat gtg tgg	2518
Thr Leu Ala Cys Gly Val Lys Asn Ala Pro Ile Lys Ala Asn Val Trp	
790 795 800	
gct aat gaa gtg gcg caa att tta ggg ggc aaa ggg ggc ggg aga ggt	2566
Ala Asn Glu Val Ala Gln Ile Leu Gly Gly Lys Gly Gly Arg Gly	
805 810 815	
gat ttt gcg agc gct gga ggc aag gat att gaa aat ttg caa gcc gca	2614
Asp Phe Ala Ser Ala Gly Gly Lys Asp Ile Glu Asn Leu Gln Ala Ala	
820 825 830	
ctc aat tta gcg aaa aat acc gct ctt aaa gct tta gag gga	2656
Leu Asn Leu Ala Lys Asn Thr Ala Leu Lys Ala Leu Glu Gly	
835 840 845	
tagcatggag cttatttttag gctctcaatc cagcactagg gcgaatctct taaaagagca	2716
tgggattaag tttgaacaaa aagcgctcta ttttgatgaa gaaagcctaa aaaccacaga	2776
ccctagggag ttg	2790
<210> 164	
<211> 847	
<212> PRT	
<213> Helicobacter pylori	
<400> 164	
Met Asp Ile Arg Asn Glu Phe Leu Gln Phe Phe Gln Asn Lys Gly His	
1 5 10 15	
Ala Val Tyr Pro Ser Met Pro Leu Val Pro Asn Asp Ala Thr Leu Leu	
20 25 30	
Phe Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile	
35 40 45	
Val Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met	
50 55 60	
Arg Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly Tyr Thr Ala	
65 70 75 80	
Arg His His Thr Leu Phe Glu Met Leu Gly Asn Phe Ser Phe Gly Asp	
85 90 95	
Tyr Phe Lys Glu Glu Ala Ile Leu Phe Ala Trp Glu Phe Val Thr Lys	
100 105 110	
Asn Leu Gly Phe Lys Pro Lys Asp Leu Tyr Ile Ser Val His Glu Lys	
115 120 125	
Asp Asp Glu Ala Val Lys Leu Trp Glu Lys Phe Val Pro Val Asp Arg	
130 135 140	
Ile Lys Lys Met Gly Asp Lys Asp Asn Phe Trp Gln Met Gly Asp Ser	
145 150 155 160	
Gly Pro Cys Gly Pro Cys Ser Glu Ile Tyr Ile Asp Gln Gly Glu Lys	
165 170 175	
His Phe Lys Gly Ser Glu Asp Tyr Phe Gly Gly Glu Gly Asp Arg Phe	
180 185 190	
Leu Glu Ile Trp Asn Leu Val Phe Met Gln Tyr Glu Arg Ser Asn Asp	
195 200 205	
Gly Val Leu Ser Pro Leu Pro Lys Pro Ser Ile Asp Thr Gly Met Gly	
210 215 220	
Leu Glu Arg Val Gln Ala Leu Leu Glu His Lys Leu Asn Asn Phe Asp	



225	Ser	Ser	Leu	Phe	Ala	Pro	Leu	Met	Glu	Glu	Ile	Ser	Glu	Leu	Thr	Ser
					245					250						255
Leu	Asp	Tyr	Ala	Ser	Glu	Phe	Gln	Pro	Ser	Phe	Arg	Val	Val	Ala	Asp	
			260						265					270		
His	Ala	Arg	Ala	Val	Ala	Phe	Leu	Leu	Ala	Gln	Gly	Val	His	Phe	Asn	
			275				280					285				
Lys	Glu	Gly	Arg	Gly	Tyr	Val	Leu	Arg	Arg	Ile	Leu	Arg	Arg	Ala	Leu	
			290				295					300				
Arg	His	Gly	Tyr	Leu	Met	Gly	Leu	Lys	Glu	Ala	Phe	Leu	Tyr	Lys	Val	
305					310					315					320	
Val	Gly	Val	Val	Cys	Glu	Gln	Phe	Ala	Asn	Thr	His	Ala	Tyr	Leu	Lys	
				325					330						335	
Glu	Ser	Lys	Glu	Met	Val	Val	Lys	Glu	Cys	Phe	Glu	Glu	Glu	Glu	His	
			340					345						350		
Phe	Leu	Glu	Thr	Leu	Glu	Ser	Gly	Met	Glu	Leu	Phe	Asn	Leu	Ser	Leu	
			355				360					365				
Lys	His	Leu	Asn	Glu	Asn	Lys	Ile	Phe	Asp	Gly	Lys	Ile	Ala	Phe	Lys	
370						375					380					
Leu	Tyr	Asp	Thr	Phe	Gly	Phe	Pro	Leu	Asp	Leu	Thr	Asn	Asp	Met	Leu	
385					390					395					400	
Arg	Ser	His	Gly	Ala	Cys	Ala	Asp	Met	Gln	Gly	Phe	Glu	Leu	Cys	Met	
				405					410						415	
Gln	Glu	Gln	Val	Lys	Arg	Ser	Lys	Ala	Ser	Trp	Lys	Gly	Lys	Gln	Asn	
			420					425						430		
Asn	Ala	Asp	Phe	Ser	Ala	Ile	Leu	Asn	Ala	Tyr	Ala	Pro	Asn	Val	Phe	
			435				440					445				
Val	Gly	Tyr	Glu	Thr	Thr	Glu	Cys	Ser	Ala	Lys	Val	Leu	Gly	Phe	Phe	
	450					455					460					
Asp	Ser	Asp	Phe	Lys	Glu	Ile	Thr	Asp	Ala	Asn	Pro	Asn	Gln	Glu	Val	
465					470					475					480	
Trp	Val	Leu	Leu	Glu	Lys	Thr	Pro	Phe	Tyr	Ala	Glu	Gly	Gly	Gly	Ala	
				485					490						495	
Ile	Gly	Asp	Arg	Gly	Ala	Leu	Phe	Lys	Asp	Asn	Gly	Glu	Val	Ala	Ile	
			500					505					510			
Val	Leu	Asp	Thr	Lys	Asn	Phe	Phe	Gly	Leu	Asn	Phe	Ser	Leu	Leu	Glu	
			515				520					525				
Ile	Lys	Lys	Ala	Leu	Lys	Lys	Gly	Asp	Gln	Val	Ile	Ala	Gln	Val	Ser	
	530					535					540					
Asp	Glu	Arg	Phe	Glu	Ile	Ala	Lys	His	His	Ser	Ala	Thr	His	Leu	Leu	
545					550					555					560	
Gln	Ser	Ala	Leu	Arg	Glu	Val	Leu	Gly	Ser	His	Val	Ser	Gln	Ala	Gly	
				565					570						575	
Ser	Leu	Val	Glu	Ser	Lys	Arg	Leu	Arg	Phe	Asp	Phe	Ser	His	Ala	Lys	
			580					585					590			
Ala	Leu	Asn	Asp	Glu	Glu	Leu	Glu	Lys	Val	Glu	Asp	Leu	Val	Asn	Ala	
			595				600					605				
Gln	Ile	Phe	Lys	His	Leu	Asn	Ser	Gln	Val	Glu	His	Met	Pro	Leu	Asn	
	610					615					620					
Gln	Ala	Lys	Asp	Lys	Gly	Ala	Leu	Ala	Leu	Phe	Ser	Glu	Lys	Tyr	Ala	
625					630					635					640	
Glu	Asn	Val	Arg	Val	Ser	Phe	Lys	Glu	Ala	Ser	Ile	Glu	Leu	Cys		
				645					650					655		
Gly	Gly	Ile	His	Val	Glu	Asn	Thr	Gly	Leu	Ile	Gly	Gly	Phe	Arg	Ile	
			660					665					670			
Val	Lys	Glu	Ser	Gly	Val	Ser	Ser	Gly	Val	Arg	Arg	Ile	Glu	Ala	Val	
			675				680					685				
Cys	Gly	Lys	Ala	Phe	Tyr	Gln	Leu	Ala	Lys	Glu	Glu	Asn	Lys	Glu	Leu	
	690					695					700					



[illegible]

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<210> 167
<211> 990
<212> DNA
<213> Helicobacter pylori
<220>
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<221> CDS  
<222> (91)...(879)

<400> 167

tccaaaacga ttgggctgaa attgaatttt ctcacgaaac aaagggctat gtgttttttaa	60
aactttttaa aaaggctgaa tgaaagaata atg aaa tta aaa tct ttt ggg gtt	114
Met Lys Leu Lys Ser Phe Gly Val	
1 5	
ttt gga aat ccc att aag cat tcc aaa tcg ccc tta atc cat aac gct	162
Phe Gly Asn Pro Ile Lys His Ser Lys Ser Pro Leu Ile His Asn Ala	
10 15 20	
tgt ttt tta act ttt caa aaa gaa tta agg ttt ttg ggg cat tac cac	210
Cys Phe Leu Thr Phe Gln Lys Glu Leu Arg Phe Leu Gly His Tyr His	
25 30 35 40	
ccc ata tta ctc cct tta gaa agc cac atc aaa agc gag ttt ttg cat	258
Pro Ile Leu Leu Pro Leu Glu Ser His Ile Lys Ser Glu Phe Leu His	
45 50 55	
ttg gga ttg agt ggg gct aat gta acc tta ccc ttt aaa gaa agg gcg	306
Leu Gly Leu Ser Gly Ala Asn Val Thr Leu Pro Phe Lys Glu Arg Ala	
60 65 70	
ttt caa gtt tgc gat aaa atc aaa ggt atc gcg ctt gaa tgc gga gcg	354
Phe Gln Val Cys Asp Lys Ile Lys Gly Ile Ala Leu Glu Cys Gly Ala	
75 80 85	
gtc aat acg ctt gtt tta gaa aat gat gag ctt gtg ggt tac aat acc	402
Val Asn Thr Leu Val Leu Glu Asn Asp Glu Leu Val Gly Tyr Asn Thr	
90 95 100	
gac gct tta ggg ttt tat ctt tct tta aag caa aaa aac tat caa aac	450
Asp Ala Leu Gly Phe Tyr Leu Ser Leu Lys Gln Lys Asn Tyr Gln Asn	
105 110 115 120	
gct ttg att tta gga gct ggg ggg agc gct aaa gcc cta gcg tgt gaa	498
Ala Leu Ile Leu Gly Ala Gly Gly Ser Ala Lys Ala Leu Ala Cys Glu	
125 130 135	
ttg aaa aaa caa ggc tta caa gtg agc gtg ttg aac cgc tct tct agg	546
Leu Lys Lys Gln Gly Leu Gln Val Ser Val Leu Asn Arg Ser Ser Arg	
140 145 150	
gga ttg gat ttt ttc caa cgc ctg ggc tgt gat tgt ttt atg gag cct	594
Gly Leu Asp Phe Phe Gln Arg Leu Gly Cys Asp Cys Phe Met Glu Pro	
155 160 165	
cct aaa agc gct ttt gat ttg att att aac gcc act tca gcg agt ttg	642
Pro Lys Ser Ala Phe Asp Leu Ile Ile Asn Ala Thr Ser Ala Ser Leu	
170 175 180	
cat aac gaa ttg cct ttg aat aaa gag gtt ttg aaa ggg tat ttt aaa	690
His Asn Glu Leu Pro Leu Asn Lys Glu Val Leu Lys Gly Tyr Phe Lys	
185 190 195 200	
gag ggc aag ctc gct tat gat ttg gcg tat ggg ttt tta acg ccc ttt	738
Glu Gly Lys Leu Ala Tyr Asp Leu Ala Tyr Gly Phe Leu Thr Pro Phe	



<211> 1080  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (47)...(1033)

<400> 169

tttttagaga gggcgtgttt gatagcgtgg atttaaagga gcaagc atg agc gct	55
Met Ser Ala	
1	
tat atc att gaa acc ctg att aaa att ttg att tta gtc gct gtt ttt	103
Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val Ala Val Phe	
5 10 15	
tcg gct tta gga ggc ttt gcc act tat att gaa agg aaa gtg tta gcc	151
Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys Val Leu Ala	
20 25 30 35	
tat ttc caa cgc cgt tta ggg cct tgt tat gtg ggg cct ttt ggg ctt	199
Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro Phe Gly Leu	
40 45 50	
ttg caa gtc gca gca gac ggc att aag ctt ttc act aaa gaa gac att	247
Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys Glu Asp Ile	
55 60 65	
atc cct caa ggc gcg aac aaa ttc att ttc acg cta gcg ccc att att	295
Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala Pro Ile Ile	
70 75 80	
gcg atg gtg agt gcg ttt gtg tcc atg gcg cct atc ccc ttt ttc cct	343
Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro Phe Phe Pro	
85 90 95	
aat ttc act ctg ttt ggc tat gag atc aag ccc ctt att tct gac atc	391
Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile Ser Asp Ile	
100 105 110 115	
aac att ggc ttt ttg ttt ttc tta gcc gtg ggt tcg gca ggg att tat	439
Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala Gly Ile Tyr	
120 125 130	
gcg cct att tta gcc ggg ctt gcc tct aat aac aaa tac tct tta att	487
Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser Leu Ile	
135 140 145	
ggc tcc gca aga gcg acg atc caa ctg ctc agc ttt gaa gtg gtc agc	535
Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val Val Ser	
150 155 160	
act tta acc att cta gcc ccc tta atg gtg gta gga tcg ctc tct tta	583
Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu Ser Leu	
165 170 175	
gtg gaa atc aat cat tac caa agc ggt ggg ttt tta gac tgg ctt gtg	631
Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp Leu Val	



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      100      105      110
Ser Asp Ile Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala
      115      120      125
Gly Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr
      130      135      140
Ser Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu
145      150      155      160
Val Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser
      165      170      175
Leu Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp
      180      185      190
Trp Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala
      195      200      205
Ser Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu
      210      215      220
Ala Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp
225      230      235      240
Gly Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe
      245      250      255
Val Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile
      260      265      270
Pro Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu
      275      280      285
Ser Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu
      290      295      300
Met Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile
305      310      315      320
Val Leu Thr Gly Ile Ile Ile Leu Ile
      325

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<210> 171  
 <211> 1280  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (48)...(1226)

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      <400> 171
taaggataaa atcaagcgat tagcccgaa ttttaagagag tattaag atg aat aaa      56
                                     Met Asn Lys
                                     1

aaa gcg tat ttt ggg gag ttt gga ggg agt ttt gtt tcg gag ttg tta      104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu
      5      10      15

gtg cct gca tta aga gaa tta gaa cag gcg ttt gat gcg tgt ttg aaa      152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys
      20      25      30      35

gat gaa aaa ttc caa aaa gaa tat ttt cgt ctt tta aag gat ttt gtg      200
Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val
      40      45      50

ggc cgt cct agc cct tta acc ttg tgt caa aat atc gtt tct aac cct      248
Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro
      55      60      65

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aaa gtc aag ctt tat tta aaa cga gag gat tta atc cat ggc ggg gcg Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His Gly Gly Ala 70 75 80	296
cat aag act aat caa gcc tta ggg caa gcc ctt tta gcg aaa aaa atg His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala Lys Lys Met 85 90 95	344
ggt aaa aca agg atc atc gct gaa aca ggc gcc ggt cag cat ggc gtg Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Val 100 105 110 115	392
gcg acg gct atc gct tgc gca tta ttg aac tta aaa tgc gtg gtt ttt Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys Val Val Phe 120 125 130	440
atg gga tct aaa gac atc aag cgc cag gaa atg aat gtt ttt aga atg Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val Phe Arg Met 135 140 145	488
cac tta tta ggc gct gaa gtg aga gag gtt aat tca ggg agc gcg acg His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly Ser Ala Thr 150 155 160	536
ctt aaa gac gct gtg aat gaa gcc tta aga gat tgg gcg agc agt tac Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala Ser Ser Tyr 165 170 175	584
aag gac acg cat tat ttg cta ggc aca gcc gcc ggg cca cac cct tac Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro His Pro Tyr 180 185 190 195	632
ccc aca atg gtt aaa acc ttt caa aaa atg ata ggc gat gag gtt aaa Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp Glu Val Lys 200 205 210	680
agc cag att tta gaa aaa gaa aac cgc ttg cct gat tat gtg atc gca Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr Val Ile Ala 215 220 225	728
tgc gtt gga ggg ggg tct aac gct ata ggg ata ttc agc gca ttt tta Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser Ala Phe Leu 230 235 240	776
aac gac aaa gaa gtt aaa ctc ata ggc gta gag ccg gcg ggt tta ggg Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala Gly Leu Gly 245 250 255	824
cta gaa acc aat aag cat ggg gcg act ttg aat aag ggg cgt gtg ggg Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly Arg Val Gly 260 265 270 275	872
att ttg cat ggg aat aaa acc tat ctt tta caa gat gat gaa ggc cag Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln 280 285 290	920
att gca gaa agc cat agc att agc gcc ggg ctt gat tat cca gga gtg Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val	968

295	300	305	
ggg cca gaa cac agc tat tta aaa gaa agt ggg cgt gcg gtt tat gaa			1016
Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu			
310	315	320	
agc gca agc gat gct gaa gcg cta gaa gcc ttc aag ttg ttg tgc caa			1064
Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln			
325	330	335	
aaa gaa ggc att atc cca gcg cta gaa agc tca cac gcc tta gcg tat			1112
Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr			
340	345	350	355
gcc tta aag ctc gct caa aaa tgc gaa gaa gaa agc atc atc gta gtg			1160
Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val			
360	365	370	
aat tta agc ggc aga ggg gat aag gat tta agc acc gtt tat aac gct			1208
Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala			
375	380	385	
tta aaa gga ggt tta aaa tgaggtatca aaacatgttt gaaaccttaa			1256
Leu Lys Gly Gly Leu Lys			
390			
aaaaacacga aaaaatggcg tttta			1280
<210> 172			
<211> 393			
<212> PRT			
<213> Helicobacter pylori			
<400> 172			
Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser			
1 5 10 15			
Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala			
20 25 30			
Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys			
35 40 45			
Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val			
50 55 60			
Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His			
65 70 75 80			
Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala			
85 90 95			
Lys Lys Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln			
100 105 110			
His Gly Val Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys			
115 120 125			
Val Val Phe Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val			
130 135 140			
Phe Arg Met His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly			
145 150 155 160			
Ser Ala Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala			
165 170 175			
Ser Ser Tyr Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro			
180 185 190			
His Pro Tyr Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp			





<222> (53)...(712)

<400> 175

tgagatcaaa cccgtagaac ttgtcaaggt aattcttgcg taaggaaata gc atg tta	58
Met Leu	
1	
ata acc acc caa cta tcc aaa cga ttt tac gcc aca ctc gct ctt tct	106
Ile Thr Thr Gln Leu Ser Lys Arg Phe Tyr Ala Thr Leu Ala Leu Ser	
5 10 15	
tgc gtg ttt tta acc atc act aac att ctt gtc aaa ggc tcg ttt atc	154
Cys Val Phe Leu Thr Ile Thr Asn Ile Leu Val Lys Gly Ser Phe Ile	
20 25 30	
aat ctt tta gca ggg ctt agt ggg gtt ttg tat gcg ttt ttt gcc gga	202
Asn Leu Leu Ala Gly Leu Ser Gly Val Leu Tyr Ala Phe Phe Ala Gly	
35 40 45 50	
gaa agg caa acg att tgc ttt gtg ttt ggt ctt gtt tat aat ttg agt	250
Glu Arg Gln Thr Ile Cys Phe Val Phe Gly Leu Val Tyr Asn Leu Ser	
55 60 65	
tac gct tat gtc gct tat cag tgg aaa tta aac gct gat gtg att tta	298
Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val Ile Leu	
70 75 80	
tgc ctt ttt ttg tat atg cca gta acg att tat ggg ctg ttc gca tgg	346
Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe Ala Trp	
85 90 95	
aaa aag aca gag cag cat gaa ggc gtt atc aag gct caa aaa ctt tcc	394
Lys Lys Thr Glu Gln His Glu Gly Val Ile Lys Ala Gln Lys Leu Ser	
100 105 110	
aaa aat tgg cgt ttt ata ctc att tta ggc gta ggg gtt tta act tgt	442
Lys Asn Trp Arg Phe Ile Leu Ile Leu Gly Val Gly Val Leu Thr Cys	
115 120 125 130	
gtg agc gct ttg ttt ttt aaa gag att aaa acg aat ttt tta tgg gca	490
Val Ser Ala Leu Phe Phe Lys Glu Ile Lys Thr Asn Phe Leu Trp Ala	
135 140 145	
gag agt ttt aat ttc gtc atc ttt att att gct ttt att tta cag gtt	538
Glu Ser Phe Asn Phe Val Ile Phe Ile Ile Ala Phe Ile Leu Gln Val	
150 155 160	
ttg cgc tat ata gaa aat tat gcg cta gta act ttg ggg aat atc gta	586
Leu Arg Tyr Ile Glu Asn Tyr Ala Leu Val Thr Leu Gly Asn Ile Val	
165 170 175	
tcc att atc gtg tgg ttt tgt att ttt caa att tct aca gag agc ttg	634
Ser Ile Ile Val Trp Phe Cys Ile Phe Gln Ile Ser Thr Glu Ser Leu	
180 185 190	
gtg caa ctc ttc aca acg atc cta tac ctt ttt att ggc ttg tat tat	682
Val Gln Leu Phe Thr Thr Ile Leu Tyr Leu Phe Ile Gly Leu Tyr Tyr	
195 200 205 210	

ttt aac cgg tgg aat aag tca tgc aag cag tgatttttagc gaatgggggag 732  
Phe Asn Arg Trp Asn Lys Ser Cys Lys Gln  
215 220

tttctctaaat ctcaaaaatg cttagacctt ttaaaaaacg ctcccttttt aatcgcatgc 792  
gatggggctg ttacctca 810

<210> 176  
<211> 220  
<212> PRT  
<213> Helicobacter pylori

<400> 176  
Met Leu Ile Thr Thr Gln Leu Ser Lys Arg Phe Tyr Ala Thr Leu Ala  
1 5 10 15  
Leu Ser Cys Val Phe Leu Thr Ile Thr Asn Ile Leu Val Lys Gly Ser  
20 25 30  
Phe Ile Asn Leu Leu Ala Gly Leu Ser Gly Val Leu Tyr Ala Phe Phe  
35 40 45  
Ala Gly Glu Arg Gln Thr Ile Cys Phe Val Phe Gly Leu Val Tyr Asn  
50 55 60  
Leu Ser Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val  
65 70 75 80  
Ile Leu Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe  
85 90 95  
Ala Trp Lys Lys Thr Glu Gln His Glu Gly Val Ile Lys Ala Gln Lys  
100 105 110  
Leu Ser Lys Asn Trp Arg Phe Ile Leu Ile Leu Gly Val Gly Val Leu  
115 120 125  
Thr Cys Val Ser Ala Leu Phe Phe Lys Glu Ile Lys Thr Asn Phe Leu  
130 135 140  
Trp Ala Glu Ser Phe Asn Phe Val Ile Phe Ile Ile Ala Phe Ile Leu  
145 150 155 160  
Gln Val Leu Arg Tyr Ile Glu Asn Tyr Ala Leu Val Thr Leu Gly Asn  
165 170 175  
Ile Val Ser Ile Ile Val Trp Phe Cys Ile Phe Gln Ile Ser Thr Glu  
180 185 190  
Ser Leu Val Gln Leu Phe Thr Thr Ile Leu Tyr Leu Phe Ile Gly Leu  
195 200 205  
Tyr Tyr Phe Asn Arg Trp Asn Lys Ser Cys Lys Gln  
210 215 220

<210> 177  
<211> 451  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (51)...(398)

<400> 177  
agtttaaaga aaagattaga aaaattagaa gataaaggag gtaacgactg atg aga 56  
Met Arg  
1

cac aaa cac gga tac cgc aag ctt ggg aga acc agc tcg cac aga aag 104  
His Lys His Gly Tyr Arg Lys Leu Gly Arg Thr Ser Ser His Arg Lys  
5 10 15



<220>  
 <221> CDS  
 <222> (36)...(1142)

<400> 179

aaaataagcg ttttgatgcc atttttggag cgatc	gtg gaa ttg agt tat tat	53
	Val Glu Leu Ser Tyr Tyr	
	1 5	
gaa att tta gaa gtg gaa aaa cac agc aac caa gag acc att aaa aag	101	
Glu Ile Leu Glu Val Glu Lys His Ser Asn Gln Glu Thr Ile Lys Lys		
10 15 20		
tct tac aga aag ctg gct tta aaa tac cac cca gac aga aac gcc ggc	149	
Ser Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro Asp Arg Asn Ala Gly		
25 30 35		
gat aaa gaa gcc gaa gaa aaa ttc aag ctc atc aat gaa gcc tat ggg	197	
Asp Lys Glu Ala Glu Glu Lys Phe Lys Leu Ile Asn Glu Ala Tyr Gly		
40 45 50		
gtg tta agc gat gaa aag aag cgg gcc tta tac gac agg tat ggt aaa	245	
Val Leu Ser Asp Glu Lys Lys Arg Ala Leu Tyr Asp Arg Tyr Gly Lys		
55 60 65 70		
aaa ggc tta aac caa gcc ggc gca agc caa ggc gat ttt tct gat ttt	293	
Lys Gly Leu Asn Gln Ala Gly Ala Ser Gln Gly Asp Phe Ser Asp Phe		
75 80 85		
ttt gaa gat tta ggc tcg ttt ttt gaa gac gct ttt ggg ttt ggc gct	341	
Phe Glu Asp Leu Gly Ser Phe Phe Glu Asp Ala Phe Gly Phe Gly Ala		
90 95 100		
agg ggg agt aaa agg caa aaa agc tct atc gca ccg gat tat ttg caa	389	
Arg Gly Ser Lys Arg Gln Lys Ser Ser Ile Ala Pro Asp Tyr Leu Gln		
105 110 115		
acc ctt gaa ttg agt ttc aaa gaa gcg gtt ttt ggc tgt aaa aaa acc	437	
Thr Leu Glu Leu Ser Phe Lys Glu Ala Val Phe Gly Cys Lys Lys Thr		
120 125 130		
att aaa gtc caa tac cag agc gtt tgt gaa agt tgc gat ggc acg ggc	485	
Ile Lys Val Gln Tyr Gln Ser Val Cys Glu Ser Cys Asp Gly Thr Gly		
135 140 145 150		
gct aaa gac aaa gcc cta gag act tgc aag caa tgc aat ggg cag ggc	533	
Ala Lys Asp Lys Ala Leu Glu Thr Cys Lys Gln Cys Asn Gly Gln Gly		
155 160 165		
cag gtg ttt atg cgt caa ggt ttt atg agt ttt gcg caa act tgt ggc	581	
Gln Val Phe Met Arg Gln Gly Phe Met Ser Phe Ala Gln Thr Cys Gly		
170 175 180		
gcg tgt caa ggc aag ggc aag atc gtt aaa acc cca tgc caa gcg tgc	629	
Ala Cys Gln Gly Lys Gly Lys Ile Val Lys Thr Pro Cys Gln Ala Cys		
185 190 195		
aag ggt aaa acc tat atc ctt aaa gat gaa gaa att gat gcg ata atc	677	
Lys Gly Lys Thr Tyr Ile Leu Lys Asp Glu Glu Ile Asp Ala Ile Ile		







Asn	Tyr	Ala	Lys	Lys	His	Phe	Ser	Gln	Cys	His	Met	Leu	Ser	Ser	Ser			
30					35					40						45		
tta	ctc	atc	tta	aac	gac	acg	gaa	tgc	ttt	aaa	aaa	aac	tac	ttg	ctt		194	
Leu	Leu	Ile	Leu	Asn	Asp	Thr	Glu	Cys	Phe	Lys	Lys	Asn	Tyr	Leu	Leu			
				50					55					60				
aat	tgg	gtc	tat	cat	gcc	ctt	gaa	tgc	gtg	cat	gaa	aaa	gat	att	agc		242	
Asn	Trp	Val	Tyr	His	Ala	Leu	Glu	Cys	Val	His	Glu	Lys	Asp	Ile	Ser			
			65					70					75					
gcg	cat	tct	tta	gaa	gag	gtt	tta	caa	aaa	agc	cac	ctg	ccc	ata	cgc		290	
Ala	His	Ser	Leu	Glu	Glu	Val	Leu	Gln	Lys	Ser	His	Leu	Pro	Ile	Arg			
		80					85					90						
atc	aaa	atc	atg	gct	caa	aac	acg	ctt	tta	gaa	aag	ata	gaa	gtg	aaa		338	
Ile	Lys	Ile	Met	Ala	Gln	Asn	Thr	Leu	Leu	Glu	Lys	Ile	Glu	Val	Lys			
	95					100					105							
gtt	tta	acc	ttt	ggg	gcg	gaa	tat	gcg	ctt	ttt	atc	acc	aaa	cac	cct		386	
Val	Leu	Thr	Phe	Gly	Ala	Glu	Tyr	Ala	Leu	Phe	Ile	Thr	Lys	His	Pro			
110					115					120					125			
atc	gcc	aag	cgg	ttt	tta	cgc	caa	aaa	ttt	agc	ggc	tgt	gtg	ttt	tta		434	
Ile	Ala	Lys	Arg	Phe	Leu	Arg	Gln	Lys	Phe	Ser	Gly	Cys	Val	Phe	Leu			
				130					135					140				
gaa	acc	caa	gat	gaa	ttg	cat	ata	aga	ggc	gat	tca	gag	cgt	ttt	tgg		482	
Glu	Thr	Gln	Asp	Glu	Leu	His	Ile	Arg	Gly	Asp	Ser	Glu	Arg	Phe	Trp			
			145					150					155					
gaa	ctc	att	gta	acg	ctc	aat	gaa	aat	aga	atc	gtc	cat	aac	gca	tgc		530	
Glu	Leu	Ile	Val	Thr	Leu	Asn	Glu	Asn	Arg	Ile	Val	His	Asn	Ala	Cys			
		160					165					170						
tta	gat	ttc	atc	tac	cct	aat	ggc	ttt	ggc	aag	gac	agc	tac	acc	act		578	
Leu	Asp	Phe	Ile	Tyr	Pro	Asn	Gly	Phe	Gly	Lys	Asp	Ser	Tyr	Thr	Thr			
	175					180					185							
atg	gct	gaa	cgc	aaa	tta	aaa	gaa	tgc	tat	aaa	acg	cta	ggg	ttt	atc		626	
Met	Ala	Glu	Arg	Lys	Leu	Lys	Glu	Cys	Tyr	Lys	Thr	Leu	Gly	Phe	Ile			
190					195					200				205				
aag	cat	gaa	gat	ttc	agc	gaa	gtc	aaa	aag	cgc	tat	tta	gaa	ttg	gct		674	
Lys	His	Glu	Asp	Phe	Ser	Glu	Val	Lys	Lys	Arg	Tyr	Leu	Glu	Leu	Ala			
				210					215					220				
aaa	acc	tac	cac	cct	gat	tta	tgc	gat	ctc	aaa	gaa	aaa	aag	gct	ctt		722	
Lys	Thr	Tyr	His	Pro	Asp	Leu	Cys	Asp	Leu	Lys	Glu	Lys	Lys	Ala	Leu			
			225					230					235					
tat	gcc	aaa	cgc	ttc	gct	atc	att	caa	gag	gcg	tat	cgc	cac	att	aaa		770	
Tyr	Ala	Lys	Arg	Phe	Ala	Ile	Ile	Gln	Glu	Ala	Tyr	Arg	His	Ile	Lys			
		240				245						250						
aaa	cac	gcc	taa	acc	cccta	aactag	ccct	aatcgc	gcgcta	g							810	
Lys	His	Ala																
		255																

<210> 182  
 <211> 256  
 <212> PRT  
 <213> Helicobacter pylori

<400> 182  
 Met Arg Val Met Ala Lys Ile Glu Leu Leu Ala Lys Phe Thr Gln Ile  
 1 5 10 15  
 Ala Leu Pro Asn Ser His Pro Leu Leu Lys Lys Val Leu Asn Tyr Ala  
 20 25 30  
 Lys Lys His Phe Ser Gln Cys His Met Leu Ser Ser Ser Leu Leu Ile  
 35 40 45  
 Leu Asn Asp Thr Glu Cys Phe Lys Lys Asn Tyr Leu Leu Asn Trp Val  
 50 55 60  
 Tyr His Ala Leu Glu Cys Val His Glu Lys Asp Ile Ser Ala His Ser  
 65 70 75 80  
 Leu Glu Glu Val Leu Gln Lys Ser His Leu Pro Ile Arg Ile Lys Ile  
 85 90 95  
 Met Ala Gln Asn Thr Leu Leu Glu Lys Ile Glu Val Lys Val Leu Thr  
 100 105 110  
 Phe Gly Ala Glu Tyr Ala Leu Phe Ile Thr Lys His Pro Ile Ala Lys  
 115 120 125  
 Arg Phe Leu Arg Gln Lys Phe Ser Gly Cys Val Phe Leu Glu Thr Gln  
 130 135 140  
 Asp Glu Leu His Ile Arg Gly Asp Ser Glu Arg Phe Trp Glu Leu Ile  
 145 150 155 160  
 Val Thr Leu Asn Glu Asn Arg Ile Val His Asn Ala Cys Leu Asp Phe  
 165 170 175  
 Ile Tyr Pro Asn Gly Phe Gly Lys Asp Ser Tyr Thr Thr Met Ala Glu  
 180 185 190  
 Arg Lys Leu Lys Glu Cys Tyr Lys Thr Leu Gly Phe Ile Lys His Glu  
 195 200 205  
 Asp Phe Ser Glu Val Lys Lys Arg Tyr Leu Glu Leu Ala Lys Thr Tyr  
 210 215 220  
 His Pro Asp Leu Cys Asp Leu Lys Glu Lys Lys Ala Leu Tyr Ala Lys  
 225 230 235 240  
 Arg Phe Ala Ile Ile Gln Glu Ala Tyr Arg His Ile Lys Lys His Ala  
 245 250 255

<210> 183  
 <211> 900  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (59)...(778)

<400> 183  
 catgatgatt attataaaat cctaacgccg catgaacaaa taggatgggt caaaaaag 58  
 atg aag tca aat aaa aag tcc aat cgt tta aga gcg att tat aga gct 106  
 Met Lys Ser Asn Lys Lys Ser Asn Arg Leu Arg Ala Ile Tyr Arg Ala  
 1 5 10 15  
 tta gtg atc gct ata gga cta gct gtt atc atc gtt ttc aat tac ttt 154  
 Leu Val Ile Ala Ile Gly Leu Ala Val Ile Ile Val Phe Asn Tyr Phe  
 20 25 30  
 aac cgc aaa aac aat aac gcc cgc tcc agc cgt agg gct tgt tcg tgc 202





Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile Lys Asp Lys Glu Arg	
55 60 65	
ttc aag cct aaa gac gct tta atg gaa att agg ggg gat ttt agc atg	294
Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg Gly Asp Phe Ser Met	
70 75 80 85	
ctt tta aag gtt gag cgc acc ctt tta aac ctt ttg caa cac agc agc	342
Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu Leu Gln His Ser Ser	
90 95 100	
ggg att gct act tta acg agc cgt ttt gta gag gct tta aat tct cat	390
Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu Ala Leu Asn Ser His	
105 110 115	
aaa gtg cgt ttg ttg gac acg aga aaa acg aga ccc ctt tta agg atc	438
Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg Pro Leu Leu Arg Ile	
120 125 130	
ttt gaa aaa tat tcc gtg ctt aat ggg gga gcg agc aac cac cgc tta	486
Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala Ser Asn His Arg Leu	
135 140 145	
ggg cta gat gac gct tta atg ctt aaa gac acg cat tta agg cat gtg	534
Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr His Leu Arg His Val	
150 155 160 165	
aaa gat ctc aaa agc ttt tta acg cat gcc aga aaa aac ttg cct ttc	582
Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe	
170 175 180	
acg gct aaa att gaa att gaa tgc gaa agc ttt gaa gag gcc aaa aac	630
Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn	
185 190 195	
gcc atg aat gcg gga gcg gat att gtg atg tgc gat aat ttg agc gtt	678
Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val	
200 205 210	
tta gag act aaa gaa att gcc gct tat aga gat gcg cat tat ccc ttt	726
Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe	
215 220 225	
gtt tta ctg gaa gcg agc ggg aac att tca cta gag agc att aac gct	774
Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala	
230 235 240 245	
tac gct aaa agc ggc gtg gat gcc att agc gta ggg gct tta atc cat	822
Tyr Ala Lys Ser Gly Val Asp Ala Ile Ser Val Gly Ala Leu Ile His	
250 255 260	
caa gcc act ttt att gac atg cac atg aaa atg gct taaagacttt	868
Gln Ala Thr Phe Ile Asp Met His Met Lys Met Ala	
265 270	
aaaaaggggt tattaacatg ctaaaagaat atttagaaag cattaagat cttacgcctg	928
aaaagaatga actcacgcac cgcccttctt tatacaactt gcttaatcag ttaaaaaacc	988
at	990

<210> 186  
 <211> 273  
 <212> PRT  
 <213> Helicobacter pylori

<400> 186  
 Met Glu Ile Arg Thr Phe Leu Glu Arg Ala Leu Lys Glu Asp Leu Gly  
 1 5 10 15  
 His Gly Asp Leu Phe Glu Arg Val Leu Glu Lys Asp Phe Lys Ala Thr  
 20 25 30  
 Ala Phe Val Arg Ala Lys Gln Glu Gly Val Phe Ser Gly Glu Lys Tyr  
 35 40 45  
 Ala Leu Glu Leu Leu Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile  
 50 55 60  
 Lys Asp Lys Glu Arg Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg  
 65 70 75 80  
 Gly Asp Phe Ser Met Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu  
 85 90 95  
 Leu Gln His Ser Ser Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu  
 100 105 110  
 Ala Leu Asn Ser His Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg  
 115 120 125  
 Pro Leu Leu Arg Ile Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala  
 130 135 140  
 Ser Asn His Arg Leu Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr  
 145 150 155 160  
 His Leu Arg His Val Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg  
 165 170 175  
 Lys Asn Leu Pro Phe Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe  
 180 185 190  
 Glu Glu Ala Lys Asn Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys  
 195 200 205  
 Asp Asn Leu Ser Val Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp  
 210 215 220  
 Ala His Tyr Pro Phe Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu  
 225 230 235 240  
 Glu Ser Ile Asn Ala Tyr Ala Lys Ser Gly Val Asp Ala Ile Ser Val  
 245 250 255  
 Gly Ala Leu Ile His Gln Ala Thr Phe Ile Asp Met His Met Lys Met  
 260 265 270  
 Ala

<210> 187  
 <211> 1153  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1100)

<400> 187  
 gatcaaacgc tacaacccta gctgtctttt agaagtggat gggggcgtga atg ata 56  
 Met Ile  
 1  
 aaa ata tct ttg aac tcc aac aag cgg gcg tgg atg tgg tgg ttt cag 104  
 Lys Ile Ser Leu Asn Ser Asn Lys Arg Ala Trp Met Trp Trp Phe Gln





Gly	Phe	Gly	Ile	Glu	Val	Ser	His	Arg	Ala	Tyr	Ala	Asp	Ala	Leu	Ala		
		245					250					255					
agc	tat	aaa	ctc	ttt	gaa	ata	tgc	ctg	tta	aac	ttg	ccc	agc	tac	atc	872	
Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu	Leu	Asn	Leu	Pro	Ser	Tyr	Ile		
	260					265					270						
aaa	acg	aca	atg	gat	ttg	att	gat	ttt	tct	aaa	tgt	gct	aac	acg	cta	920	
Lys	Thr	Thr	Met	Asp	Leu	Ile	Asp	Phe	Ser	Lys	Cys	Ala	Asn	Thr	Leu		
275					280					285					290		
atc	aaa	aga	ccc	cca	aaa	gcc	aga	tac	caa	gag	att	cca	tcg	cca	ttt	968	
Ile	Lys	Arg	Pro	Pro	Lys	Ala	Arg	Tyr	Gln	Glu	Ile	Pro	Ser	Pro	Phe		
			295						300					305			
tct	ctt	ttt	gaa	aag	aca	aag	ggc	ttg	ttc	aat	cat	aaa	agc	aac	cag	1016	
Ser	Leu	Phe	Glu	Lys	Thr	Lys	Gly	Leu	Phe	Asn	His	Lys	Ser	Asn	Gln		
			310					315					320				
tta	aac	gaa	agc	tgt	tta	atg	ggg	ttt	atg	ggg	act	gaa	att	tta	gca	1064	
Leu	Asn	Glu	Ser	Cys	Leu	Met	Gly	Phe	Met	Gly	Thr	Glu	Ile	Leu	Ala		
		325					330					335					
tct	cta	ttt	gat	act	ttt	gaa	tgt	tgc	cta	gta	ttt	tgattttatc				1110	
Ser	Leu	Phe	Asp	Thr	Phe	Glu	Cys	Cys	Leu	Val	Phe						
	340					345					350						
ggttacttcg	cactcatcgt	atatcttttt	gtattcttgt	atg												1153	
		<210>	188														
		<211>	350														
		<212>	PRT														
		<213>	Helicobacter pylori														
		<400>	188														
Met	Ile	Lys	Ile	Ser	Leu	Asn	Ser	Asn	Lys	Arg	Ala	Trp	Met	Trp	Trp		
1				5					10					15			
Phe	Gln	Gly	Val	Ile	Phe	Leu	Asn	Pro	Lys	Ile	Val	Ser	Trp	Leu	Leu		
			20					25					30				
Lys	Ala	Tyr	Arg	Met	Ser	Asp	Asn	Leu	Leu	His	Lys	Asp	Ile	Gln	Ala		
		35					40					45					
Leu	Ile	Ala	Arg	Leu	Lys	Arg	Gln	Asp	Leu	Ser	Leu	Gly	Met	Leu	Glu		
	50					55					60						
Lys	Ser	Leu	Ser	Arg	Leu	Ile	His	Asp	Glu	Ile	Asn	Leu	Glu	Tyr	Leu		
65				70						75					80		
Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser	Glu	Asn	Leu	Ile	Thr		
			85					90						95			
Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu	Val	Phe					

Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg Tyr Phe Val Glu Lys  
 195 200 205  
 Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys Thr Leu Asp Leu Ser  
 210 215 220  
 Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu  
 225 230 235 240  
 Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg Ala Tyr Ala Asp Ala  
 245 250 255  
 Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu Leu Asn Leu Pro Ser  
 260 265 270  
 Tyr Ile Lys Thr Thr Met Asp Leu Ile Asp Phe Ser Lys Cys Ala Asn  
 275 280 285  
 Thr Leu Ile Lys Arg Pro Pro Lys Ala Arg Tyr Gln Glu Ile Pro Ser  
 290 295 300  
 Pro Phe Ser Leu Phe Glu Lys Thr Lys Gly Leu Phe Asn His Lys Ser  
 305 310 315 320  
 Asn Gln Leu Asn Glu Ser Cys Leu Met Gly Phe Met Gly Thr Glu Ile  
 325 330 335  
 Leu Ala Ser Leu Phe Asp Thr Phe Glu Cys Cys Leu Val Phe  
 340 345 350

<210> 189  
 <211> 990  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (52)...(864)

<400> 189  
 aaaaacactt tttaatgtta taatctatcc taaacaatat aaggggtttt t atg gca 57  
 Met Ala  
 1  
 aaa att gaa agc aat gat tcc cac cta aga ggt att tta aaa gac gaa 105  
 Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys Asp Glu  
 5 10 15  
 ctc tac tat caa atc ccc atc tac caa cgc cct tat caa tgg aca gaa 153  
 Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp Thr Glu  
 20 25 30  
 gaa aac tgc gaa aaa ctt tta gac gat ttg ttt ttt aat tat gaa gat 201  
 Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr Glu Asp  
 35 40 45 50  
 gac aga gaa ggc gat tat ttt tgc ggc tca tta gtc tta att gca atc 249  
 Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile Ala Ile  
 55 60 65  
 agc aaa gat tct aaa gcc aca acc tat gat gtt gta gat ggc cag caa 297  
 Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly Gln Gln  
 70 75 80  
 cgc tta agc act ttc att ctg ctt gca aaa gtt tta gcc gat ctt tat 345  
 Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp Leu Tyr  
 85 90 95

aat gat tgt tta gac cct aag aat tta gaa cat tta caa gag ggt tgg	393
Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu Gly Trp	
100 105 110	
aaa gat agg cat aca gaa aga aaa cga ctg agt ttt aac act ata ggg	441
Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr Ile Gly	
115 120 125 130	
tct aac gct gaa tat gat ttt caa gat gca tta gaa cat ttc aac gac	489
Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe Asn Asp	
135 140 145	
tct caa gca agc aag aat aaa aat aat aag aac aat tac cta aaa aat	537
Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu Lys Asn	
150 155 160	
gcg atc tgt tta aaa gac tat ctc atg aaa aaa gag att aaa aac att	585
Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys Asn Ile	
165 170 175	
aac gat ttc att gag tgg ctg tat tct aat gtt aaa ttt atc acc atc	633
Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile Thr Ile	
180 185 190	
att tgc cca aac ata gac aag gca tta agg att ttt aat gtt tta aac	681
Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val Leu Asn	
195 200 205 210	
gct agg ggt ttg cct ttg aat gcg aca gat att ttt aag ggg gaa tta	729
Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly Glu Leu	
215 220 225	
tta aaa cac gct aaa gag cat gag cga gaa gaa ttt gtg tct cgt tgg	777
Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser Arg Trp	
230 235 240	
aac gcc tta agc caa aaa tgc tcg gac aat gat tta aca atg gag aca	825
Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met Glu Thr	
245 250 255	
tta ttc agt tgg tat aac cta tct caa tcc ggt aac ttc tagagacaaa	874
Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe	
260 265 270	
atggaaaaag agctcgttac ttggttcaac atacttaaca aacccccctt agaatacctt	934
aagggcgtag aggattttta caacgcttat ggtgaggtgt tagaaatgca agatcg	990

<210> 190

<211> 271

<212> PRT

<213> Helicobacter pylori

<400> 190

Met Ala Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys	
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Asp Glu Leu Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp	
20 25 30	
Thr Glu Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr	
35 40 45	

Glu Asp Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile  
50 55 60  
Ala Ile Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly  
65 70 75 80  
Gln Gln Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp  
85 90 95  
Leu Tyr Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu  
100 105 110  
Gly Trp Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr  
115 120 125  
Ile Gly Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe  
130 135 140  
Asn Asp Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu  
145 150 155 160  
Lys Asn Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys  
165 170 175  
Asn Ile Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile  
180 185 190  
Thr Ile Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val  
195 200 205  
Leu Asn Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly  
210 215 220  
Glu Leu Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser  
225 230 235 240  
Arg Trp Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met  
245 250 255  
Glu Thr Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe  
260 265 270

<210> 191  
<211> 283  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (51)...(230)

<400> 191

ccctagaatg cgtgcttttg gctaaggaat ttttgcctaa cgctaggcctt atg gtg 56  
Met Val  
1

gct ggg ggg cgt gaa gtg gtg ttt aaa gat aat gac aaa aag gaa gcc 104  
Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys Glu Ala  
5 10 15

aag ctt ttt gaa tac ggc atc aat gcg gtg gtg cta ggg gac tat ttg 152  
Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp Tyr Leu  
20 25 30

acc acc aaa ggc aaa gcc cct aaa aaa gat ata gaa aaa ctg ctc tct 200  
Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu Leu Ser  
35 40 45 50

tat ggc ttg aca atg gcg aca agc tgt cat taatgagaga acttttttaa 250  
Tyr Gly Leu Thr Met Ala Thr Ser Cys His  
55 60

agcggttagag gggttttttcg ccttcttaga atg

283

<210> 192  
 <211> 60  
 <212> PRT  
 <213> Helicobacter pylori

<400> 192  
 Met Val Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys  
 1 5 10 15  
 Glu Ala Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp  
 20 25 30  
 Tyr Leu Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu  
 35 40 45  
 Leu Ser Tyr Gly Leu Thr Met Ala Thr Ser Cys His  
 50 55 60

<210> 193  
 <211> 478  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(425)

<400> 193  
 cacttggttg gagtgcctat aggcataata agtcctgttt ctatttttaa tgg tgg 56  
 Trp Trp  
 1  
 tat gat aac aat gtc aac tta cag ctt ttt tat gga ttt tta cac aat 104  
 Tyr Asp Asn Asn Val Asn Leu Gln Leu Phe Tyr Gly Phe Leu His Asn  
 5 10 15  
 gtg tat gaa aat gag aag ttt ttc atc ggt tat ttt ata ggg gct ggg 152  
 Val Tyr Glu Asn Glu Lys Phe Phe Ile Gly Tyr Phe Ile Gly Ala Gly  
 20 25 30  
 cta ggg ggt gag agc gta aca ccc aat gtt ctt aaa gat ttt ggt aat 200  
 Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe Gly Asn  
 35 40 45 50  
 atg tta gcg caa tta gtg caa ttt cag ggc tat ggc tca cta ggg cta 248  
 Met Leu Ala Gln Leu Val Gln Phe Gln Gly Tyr Gly Ser Leu Gly Leu  
 55 60 65  
 agg atg ggc gat aaa cac cac acg cta gaa ttg agc acg agc gtt cat 296  
 Arg Met Gly Asp Lys His His Thr Leu Glu Leu Ser Thr Ser Val His  
 70 75 80  
 ggc gac gct cct agt tgt tct tta aaa aag cta aag agt tgc gaa agt 344  
 Gly Asp Ala Pro Ser Cys Ser Leu Lys Lys Leu Lys Ser Cys Glu Ser  
 85 90 95  
 gcg agg gtt tta caa gca aaa atc cct agg ggc att ttt gaa agc tat 392  
 Ala Arg Val Leu Gln Ala Lys Ile Pro Arg Gly Ile Phe Glu Ser Tyr  
 100 105 110



cca aac aac cac cac aaa caa aaa cat gcc aaa aca cga aat tac gcc	298
Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn Tyr Ala	
70 75 80	
caa gaa gaa ttg gat agc aac aaa gta gag ggc gtt acg gaa att ttg	346
Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu Ile Leu	
85 90 95	
cat gtg aat gag aga ggg act tta ggc ttt cat aag gag tta aaa aag	394
His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu Lys Lys	
100 105 110	
ggc gtt gaa gcg aat aac aag atc caa gtg gag cat tta aac ccg cat	442
Gly Val Glu Ala Asn Asn Lys Ile Gln Val Glu His Leu Asn Pro His	
115 120 125 130	
tat aag atg aac tta aac tct aaa gcg agc gtt aaa atc acg cct tta	490
Tyr Lys Met Asn Leu Asn Ser Lys Ala Ser Val Lys Ile Thr Pro Leu	
135 140 145	
ggg ggc ttg ggt gag att ggg ggg aac atg atg gtc att gaa acc cca	538
Gly Gly Leu Gly Glu Ile Gly Gly Asn Met Met Val Ile Glu Thr Pro	
150 155 160	
aaa agc gcg atc gtg att gat gcg ggc atg agc ttc cct aaa gag ggg	586
Lys Ser Ala Ile Val Ile Asp Ala Gly Met Ser Phe Pro Lys Glu Gly	
165 170 175	
ctc ttt ggc gtg gat att tta atc ccg gat ttt tcc tac ttg cac caa	634
Leu Phe Gly Val Asp Ile Leu Ile Pro Asp Phe Ser Tyr Leu His Gln	
180 185 190	
atc aag gac aaa atc gct ggc att atc atc acc cat gcc cat gaa gat	682
Ile Lys Asp Lys Ile Ala Gly Ile Ile Ile Thr His Ala His Glu Asp	
195 200 205 210	
cac ata ggg gcc acg cct tat ttg ttt aaa gag ctg caa ttc ccc ctt	730
His Ile Gly Ala Thr Pro Tyr Leu Phe Lys Glu Leu Gln Phe Pro Leu	
215 220 225	
tat ggc acg ccc ttg agt ttg ggg ctg att ggg agc aag ttt gat gaa	778
Tyr Gly Thr Pro Leu Ser Leu Gly Leu Ile Gly Ser Lys Phe Asp Glu	
230 235 240	
cat ggt ttg aaa aaa tac cgc tcg tat ttt aaa atc gta gaa aag cgc	826
His Gly Leu Lys Lys Tyr Arg Ser Tyr Phe Lys Ile Val Glu Lys Arg	
245 250 255	
tgt ccc att agc gtg ggc gaa ttt atc att gaa tgg atc cac atc acg	874
Cys Pro Ile Ser Val Gly Glu Phe Ile Ile Glu Trp Ile His Ile Thr	
260 265 270	
cat tct atc att gac agc agc gct tta gcg atc caa act aaa gcc gga	922
His Ser Ile Ile Asp Ser Ser Ala Leu Ala Ile Gln Thr Lys Ala Gly	
275 280 285 290	
acg atc atc cac acc ggc gat ttt aaa atc gat cac acc ccg gtg gat	970
Thr Ile Ile His Thr Gly Asp Phe Lys Ile Asp His Thr Pro Val Asp	
295 300 305	



aat ttg ccc acg gat ttg tat cgt tta gcg cac tat ggc gaa aag ggg Asn Leu Pro Thr Asp Leu Tyr Arg Leu Ala His Tyr Gly Glu Lys Gly 310 315 320	1018
gtg atg ctt ctt tta agc gat tcc acc aac tcc cat aaa tcc ggg act Val Met Leu Leu Leu Ser Asp Ser Thr Asn Ser His Lys Ser Gly Thr 325 330 335	1066
acg ccg agt gaa agc acc ata gcg ccg gct ttt gat acc ctt ttt aaa Thr Pro Ser Glu Ser Thr Ile Ala Pro Ala Phe Asp Thr Leu Phe Lys 340 345 350	1114
gaa gcg caa ggg agg gtg att atg agc acc ttc tct agc aat atc cac Glu Ala Gln Gly Arg Val Ile Met Ser Thr Phe Ser Ser Asn Ile His 355 360 365 370	1162
cgg gtc tat caa gcc ata caa tac gcg att aaa tac aac cgc aag atc Arg Val Tyr Gln Ala Ile Gln Tyr Gly Ile Lys Tyr Asn Arg Lys Ile 375 380 385	1210
gct gtg atc ggg cgc tct atg gaa aaa aac cta gac atc gct aga gaa Ala Val Ile Gly Arg Ser Met Glu Lys Asn Leu Asp Ile Ala Arg Glu 390 395 400	1258
ttg ggc tat atc cat ttg cct tat caa tct ttt att gaa gcc aat gaa Leu Gly Tyr Ile His Leu Pro Tyr Gln Ser Phe Ile Glu Ala Asn Glu 405 410 415	1306
gtc gcc aaa tac ccg gac aat gaa atc tta atc gta acg acc ggc tca Val Ala Lys Tyr Pro Asp Asn Glu Ile Leu Ile Val Thr Thr Gly Ser 420 425 430	1354
caa ggc gaa acc atg agc gcg ctt tat cgc atg gcg act gat gaa cac Gln Gly Glu Thr Met Ser Ala Leu Tyr Arg Met Ala Thr Asp Glu His 435 440 445 450	1402
cgt cat att tct atc aaa ccc aac gat tta gtc atc att tcc gct aaa Arg His Ile Ser Ile Lys Pro Asn Asp Leu Val Ile Ile Ser Ala Lys 455 460 465	1450
gcc att cct ggc aat gaa gcg agc gtt tca gcg gtg ttg aat ttc ttg Ala Ile Pro Gly Asn Glu Ala Ser Val Ser Ala Val Leu Asn Phe Leu 470 475 480	1498
atc aaa aaa gaa gct aaa gtg gct tat caa gaa ttt gac aat atc cat Ile Lys Lys Glu Ala Lys Val Ala Tyr Gln Glu Phe Asp Asn Ile His 485 490 495	1546
gtg agc ggg cat gcc gcc caa gaa gag caa aag ctc atg tta aga ctc Val Ser Gly His Ala Ala Gln Glu Glu Gln Lys Leu Met Leu Arg Leu 500 505 510	1594
att aag cct aag ttt ttc tta ccc gtg cat ggg gaa tat aac cat gtc Ile Lys Pro Lys Phe Phe Leu Pro Val His Gly Glu Tyr Asn His Val 515 520 525 530	1642
gcg cgc cac aaa caa acc gct att tct tgc gga gtg cct gaa aaa aat Ala Arg His Lys Gln Thr Ala Ile Ser Cys Gly Val Pro Glu Lys Asn	1690

535	540	545	
atc tat tta atg gag gat ggc gat cag gtg gag gtt ggc cct gcg ttc Ile Tyr Leu Met Glu Asp Gly Asp Gln Val Glu Val Gly Pro Ala Phe 550 555 560			1738
atc aaa aaa gtc ggc acg att aaa agc ggg aaa agc tat gtg gat aac Ile Lys Lys Val Gly Thr Ile Lys Ser Gly Lys Ser Tyr Val Asp Asn 565 570 575			1786
caa agc aat ttg agt att gat aca agc atc gtg caa caa aga gaa gaa Gln Ser Asn Leu Ser Ile Asp Thr Ser Ile Val Gln Gln Arg Glu Glu 580 585 590			1834
gtc gct agc gcc ggg gtg ttt gtg gct acg att ttt gtg aat aaa aac Val Ala Ser Ala Gly Val Phe Val Ala Thr Ile Phe Val Asn Lys Asn 595 600 605 610			1882
aag caa gcg ctt tta gaa agc tct caa ttt tcc agt tta ggg ctt gtg Lys Gln Ala Leu Leu Glu Ser Ser Gln Phe Ser Ser Leu Gly Leu Val 615 620 625			1930
ggg ttc aaa gat gaa aag cct ttg atc aaa gaa att caa ggg ggc tta Gly Phe Lys Asp Glu Lys Pro Leu Ile Lys Glu Ile Gln Gly Gly Leu 630 635 640			1978
gag gtg tta ttg aaa tcc agc aac gcc gaa att ttg aat aac cct aaa Glu Val Leu Leu Lys Ser Ser Asn Ala Glu Ile Leu Asn Asn Pro Lys 645 650 655			2026
aaa tta gaa gat cac act cgt aat ttc atc aga aaa gcg ctc ttt aaa Lys Leu Glu Asp His Thr Arg Asn Phe Ile Arg Lys Ala Leu Phe Lys 660 665 670			2074
aag ttt aga aaa tac ccg gct atc att tgt cat gcc cat tct ttt Lys Phe Arg Lys Tyr Pro Ala Ile Ile Cys His Ala His Ser Phe 675 680 685			2119
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Asn Ser Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr 20 25 30			
Asn Arg Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr 35 40 45			
Ser Asn His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn 50 55 60			
Lys Lys Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn 65 70 75 80			
Tyr Ala Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu 85 90 95			
Ile Leu His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu			

Lys	Lys	Gly	Val	Glu	Ala	Asn	Asn	Lys	Ile	Gln	Val	Glu	His	Leu	Asn
		115					120					125			
Pro	His	Tyr	Lys	Met	Asn	Leu	Asn	Ser	Lys	Ala	Ser	Val	Lys	Ile	Thr
	130					135					140				
Pro	Leu	Gly	Gly	Leu	Gly	Glu	Ile	Gly	Gly	Asn	Met	Met	Val	Ile	Glu
145					150					155					160
Thr	Pro	Lys	Ser	Ala	Ile	Val	Ile	Asp	Ala	Gly	Met	Ser	Phe	Pro	Lys
				165					170					175	
Glu	Gly	Leu	Phe	Gly	Val	Asp	Ile	Leu	Ile	Pro	Asp	Phe	Ser	Tyr	Leu
			180					185					190		
His	Gln	Ile	Lys	Asp	Lys	Ile	Ala	Gly	Ile	Ile	Ile	Thr	His	Ala	His
		195					200					205			
Glu	Asp	His	Ile	Gly	Ala	Thr	Pro	Tyr	Leu	Phe	Lys	Glu	Leu	Gln	Phe
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Pro	Leu	Tyr	Gly	Thr	Pro	Leu	Ser	Leu	Gly	Leu	Ile	Gly	Ser	Lys	Phe
225					230					235					240
Asp	Glu	His	Gly	Leu	Lys	Lys	Tyr	Arg	Ser	Tyr	Phe	Lys	Ile	Val	Glu
				245					250					255	
Lys	Arg	Cys	Pro	Ile	Ser	Val	Gly	Glu	Phe	Ile	Ile	Glu	Trp	Ile	His
			260					265					270		
Ile	Thr	His	Ser	Ile	Ile	Asp	Ser	Ser	Ala	Leu	Ala	Ile	Gln	Thr	Lys
		275					280						285		
Ala	Gly	Thr	Ile	Ile	His	Thr	Gly	Asp	Phe	Lys	Ile	Asp	His	Thr	Pro
	290					295					300				
Val	Asp	Asn	Leu	Pro	Thr	Asp	Leu	Tyr	Arg	Leu	Ala	His	Tyr	Gly	Glu
305					310					315					320
Lys	Gly	Val	Met	Leu	Leu	Leu	Ser	Asp	Ser	Thr	Asn	Ser	His	Lys	Ser
				325					330					335	
Gly	Thr	Thr	Pro	Ser	Glu	Ser	Thr	Ile	Ala	Pro	Ala	Phe	Asp	Thr	Leu
			340					345					350		
Phe	Lys	Glu	Ala	Gln	Gly	Arg	Val	Ile	Met	Ser	Thr	Phe	Ser	Ser	Asn
		355					360					365			
Ile	His	Arg	Val	Tyr	Gln	Ala	Ile	Gln	Tyr	Gly	Ile	Lys	Tyr	Asn	Arg
	370					375						380			
Lys	Ile	Ala	Val	Ile	Gly	Arg	Ser	Met	Glu	Lys	Asn	Leu	Asp	Ile	Ala
385					390					395					400
Arg	Glu	Leu	Gly	Tyr	Ile	His	Leu	Pro	Tyr	Gln	Ser	Phe	Ile	Glu	Ala
				405					410					415	
Asn	Glu	Val	Ala	Lys	Tyr	Pro	Asp	Asn	Glu	Ile	Leu	Ile	Val	Thr	Thr
			420					425					430		
Gly	Ser	Gln	Gly	Glu	Thr	Met	Ser	Ala	Leu	Tyr	Arg	Met	Ala	Thr	Asp
		435					440					445			
Glu	His	Arg	His	Ile	Ser	Ile	Lys	Pro	Asn	Asp	Leu	Val	Ile	Ile	Ser
	450					455					460				
Ala	Lys	Ala	Ile	Pro	Gly	Asn	Glu	Ala	Ser	Val	Ser	Ala	Val	Leu	Asn
465					470					475					480
Phe	Leu	Ile	Lys	Lys	Glu	Ala	Lys	Val	Ala	Tyr	Gln	Glu	Phe	Asp	Asn
				485					490					495	
Ile	His	Val	Ser	Gly	His	Ala	Ala	Gln	Glu	Glu	Gln	Lys	Leu	Met	Leu
			500					505					510		
Arg	Leu	Ile	Lys	Pro	Lys	Phe	Phe	Leu	Pro	Val	His	Gly	Glu	Tyr	Asn
		515					520					525			
His	Val	Ala	Arg	His	Lys	Gln	Thr	Ala	Ile	Ser	Cys	Gly	Val	Pro	Glu
	530					535					540				
Lys	Asn	Ile	Tyr	Leu	Met	Glu	Asp	Gly	Asp	Gln	Val	Glu	Val	Gly	Pro
545					550					555					560
Ala	Phe	Ile	Lys	Lys	Val	Gly	Thr	Ile	Lys	Ser	Gly	Lys	Ser	Tyr	Val
				565					570					575	

Asp	Asn	Gln	Ser	Asn	Leu	Ser	Ile	Asp	Thr	Ser	Ile	Val	Gln	Gln	Arg
			580					585					590		
Glu	Glu	Val	Ala	Ser	Ala	Gly	Val	Phe	Val	Ala	Thr	Ile	Phe	Val	Asn
		595					600					605			
Lys	Asn	Lys	Gln	Ala	Leu	Leu	Glu	Ser	Ser	Gln	Phe	Ser	Ser	Leu	Gly
	610					615					620				
Leu	Val	Gly	Phe	Lys	Asp	Glu	Lys	Pro	Leu	Ile	Lys	Glu	Ile	Gln	Gly
625					630					635					640
Gly	Leu	Glu	Val	Leu	Leu	Lys	Ser	Ser	Asn	Ala	Glu	Ile	Leu	Asn	Asn
			645						650					655	
Pro	Lys	Lys	Leu	Glu	Asp	His	Thr	Arg	Asn	Phe	Ile	Arg	Lys	Ala	Leu
			660					665					670		
Phe	Lys	Lys	Phe	Arg	Lys	Tyr	Pro	Ala	Ile	Ile	Cys	His	Ala	His	Ser
		675					680					685			
Phe															

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<220>  
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ttc agc aac ctc aat gaa gaa ccc tta aaa aac caa atc aaa gcc gag Phe Ser Asn Leu Asn Glu Glu Pro Leu Lys Asn Gln Ile Lys Ala Glu <div style="text-align: right; margin-right: 100px;">5</div> <div style="text-align: right; margin-right: 100px;">10</div> <div style="text-align: right; margin-right: 100px;">15</div> <div style="text-align: right; margin-right: 100px;">20</div>															105
ttt ttt aag gat aag aaa ttc ctt tat agc ggg gat aaa ata gat ttc Phe Phe Lys Asp Lys Lys Phe Leu Tyr Ser Gly Asp Lys Ile Asp Phe <div style="text-align: right; margin-right: 100px;">25</div> <div style="text-align: right; margin-right: 100px;">30</div> <div style="text-align: right; margin-right: 100px;">35</div>															153
atg cta agc tat aag cat tct aac gcc acc tta ccc att tta tgg ggc Met Leu Ser Tyr Lys His Ser Asn Ala Thr Leu Pro Ile Leu Trp Gly <div style="text-align: right; margin-right: 100px;">40</div> <div style="text-align: right; margin-right: 100px;">45</div> <div style="text-align: right; margin-right: 100px;">50</div>															201
gaa gct aaa agg ggc gat ttt gat gat ttg gac aaa gct ttc acg caa Glu Ala Lys Arg Gly Asp Phe Asp Asp Leu Asp Lys Ala Phe Thr Gln <div style="text-align: right; margin-right: 100px;">55</div> <div style="text-align: right; margin-right: 100px;">60</div> <div style="text-align: right; margin-right: 100px;">65</div>															249
ctt ctt tta acc ata ggc aag cac agg ctt tat acc cac cac aca cca Leu Leu Leu Thr Ile Gly Lys His Arg Leu Tyr Thr His His Thr Pro <div style="text-align: right; margin-right: 100px;">70</div> <div style="text-align: right; margin-right: 100px;">75</div> <div style="text-align: right; margin-right: 100px;">80</div>															297
cct tat ttg tgc gct ttt aac gct ttt aaa atg gaa ttt atc gcc ttt Pro Tyr Leu Cys Ala Phe Asn Ala Phe Lys Met Glu Phe Ile Ala Phe <div style="text-align: right; margin-right: 100px;">85</div> <div style="text-align: right; margin-right: 100px;">90</div> <div style="text-align: right; margin-right: 100px;">95</div> <div style="text-align: right; margin-right: 100px;">100</div>															345
gat gac acg atc aca agc ttt ttt tat aaa agc gat ata gat ttt tct Asp Asp Thr Ile Thr Ser Phe Phe Tyr Lys Ser Asp Ile Asp Phe Ser <div style="text-align: right; margin-right: 100px;">105</div> <div style="text-align: right; margin-right: 100px;">110</div> <div style="text-align: right; margin-right: 100px;">115</div>															393

atc acc cca agc aac cac aac aca gaa ggt ttt aaa cat gct tta gac Ile Thr Pro Ser Asn His Asn Thr Glu Gly Phe Lys His Ala Leu Asp 120 125 130	441
gcg ttt aaa gcc atg agc aaa tcc cat aaa ttc gtt ttt gac ttt aaa Ala Phe Lys Ala Met Ser Lys Ser His Lys Phe Val Phe Asp Phe Lys 135 140 145	489
acc caa agc caa gaa tgc aaa gaa ttt atc aaa aac cgt tta aat tct Thr Gln Ser Gln Glu Cys Lys Glu Phe Ile Lys Asn Arg Leu Asn Ser 150 155 160	537
agc cat tta ctc agc aaa atc caa att gac aaa aac aat ttc ttt acg Ser His Leu Leu Ser Lys Ile Gln Ile Asp Lys Asn Asn Phe Phe Thr 165 170 175 180	585
atc tat caa aag tgg ctt gaa att gtc aaa ccc acc att gac ata aat Ile Tyr Gln Lys Trp Leu Glu Ile Val Lys Pro Thr Ile Asp Ile Asn 185 190 195	633
tgg gag gtg gct aaa act aaa gac att tta gac gca gac tat tat tta Trp Glu Val Ala Lys Thr Lys Asp Ile Leu Asp Ala Asp Tyr Tyr Leu 200 205 210	681
gcg gat ttg ctt agc gat ggc gat aaa acc att att gag aaa ttg cac Ala Asp Leu Leu Ser Asp Gly Asp Lys Thr Ile Ile Glu Lys Leu His 215 220 225	729
acg att tta aga tcg agc cat tat aaa ttg aat agg ggt gtg aat gaa Thr Ile Leu Arg Ser Ser His Tyr Lys Leu Asn Arg Gly Val Asn Glu 230 235 240	777
tta ggc aaa atg gat ttt atg gaa gtt ggt ttc aca gac agc caa caa Leu Gly Lys Met Asp Phe Met Glu Val Gly Phe Thr Asp Ser Gln Gln 245 250 255 260	825
gcc cat caa gaa ttt tgg agc gtt tat gaa cga ccg cct aaa aga gaa Ala His Gln Glu Phe Trp Ser Val Tyr Glu Arg Pro Pro Lys Arg Glu 265 270 275	873
ttt caa gcc tct att tta gag cgg cgc gac ttg tta gta cca agc gat Phe Gln Ala Ser Ile Leu Glu Arg Arg Asp Leu Leu Val Pro Ser Asp 280 285 290	921
gtg aga gaa agg aaa ggg gcg ttt ttc acc cct aaa atc tgg gta gaa Val Arg Glu Arg Lys Gly Ala Phe Phe Thr Pro Lys Ile Trp Val Glu 295 300 305	969
aag agt caa gaa tat tta gct aaa gct ttg ggg caa gat tat caa gag Lys Ser Gln Glu Tyr Leu Ala Lys Ala Leu Gly Gln Asp Tyr Gln Glu 310 315 320	1017
gat tgt atc att tgg gat tgc gct ggg ggg act ggg aat ttg ctt cga Asp Cys Ile Ile Trp Asp Cys Ala Gly Gly Thr Gly Asn Leu Leu Arg 325 330 335 340	1065
ggt tta ttg aat aag gct aat ttg tat cta tcc act tta gat cat aac Gly Leu Leu Asn Lys Ala Asn Leu Tyr Leu Ser Thr Leu Asp His Asn 345 350 355	1113



585					590					595						
gcc Ala	ccc Pro	ttt Phe	gaa Glu 600	acc Thr	cct Pro	tta Leu	cac His	act Thr 605	gtt Val	agt Ser	tta Leu	gaa Glu	ata Ile 610	ttt Phe	gat Asp	1881
agt Ser	ttc Phe	ggc Gly 615	gga Gly	ttt Phe	tta Leu	ggc Gly	agt Ser 620	aaa Lys	aaa Lys	ata Ile	tac Tyr	act Thr 625	cac His	aca Thr	ata Ile	1929
gac Asp	aaa Lys 630	atg Met	ctt Leu	act Thr	tta Leu	gcg Ala 635	gat Asp	tat Tyr	tta Leu	caa Gln	aag Lys 640	ttt Phe	cag Gln	cca Pro	aca Thr	1977
aaa Lys 645	aga Arg	gac Asp	act Thr	att Ile	ttt Phe 650	ggc Gly	tat Tyr	tta Leu	gat Asp 655	cct Pro	ggt Gly	cgc Arg	aat Asn	agt Ser	ttt Phe 660	2025
caa Gln	cat His	caa Gln	aat Asn	cta Leu 665	att Ile	cat His	att Ile	agc Ser	att Ile 670	att Ile	gac Asp	aaa Lys	tca Ser	aaa Lys 675	caa Gln	2073
tcg Ser	cat His	gta Val	aaa Lys 680	tat Tyr	ttt Phe	cca Pro	atc Ile	att Ile 685	gca Ala	act Thr	aca Thr	att Ile	ttg Leu 690	ttg Leu	gta Val	2121
tct Ser	gta Val	ttt Phe 695	ttc Phe	tcc Ser	atc Ile	cgc Arg	cat His 700	tgc Cys	atc Ile	aaa Lys	gcc Ala	aca Thr 705	tgg Trp	caa Gln	aac Asn	2169
gat Asp	agg Arg 710	gat Asp	caa Gln	ttt Phe	tac Tyr	gcc Ala 715	ccc Pro	tat Tyr	gac Asp	gat Asp	gcg Ala 720	ttc Phe	caa Gln	gac Asp	gac Asp	2217
agc Ser 725	gag Glu	ttt Phe	aaa Lys	aac Asn	aat Asn 730	tgt Cys	ttg Leu	att Ile	ttc Phe	atg Met 735	ctt Leu	ttt Phe	cac His	acc Thr	cag Gln 740	2265
aac Asn	cgc Arg	atc Ile	act Thr	acc Thr 745	gct Ala	caa Gln	ggg Gly	act Thr 750	aac Asn	cat His	ttt Phe	atc Ile	ccc Pro	ttt Phe 755	agc Ser	2313
gaa Glu	act Thr	gaa Glu	gtc Val 760	aat Asn	gcc Ala	aaa Lys	gaa Glu	aga Arg 765	tat Tyr	tct Ser	agc Ser	cac His	gct Ala 770	cta Leu	tta Leu	2361
gag Glu	ttt Phe	tta Leu 775	aaa Lys	ggc Gly	gaa Glu	atc Ile	aaa Lys 780	gaa Glu	ctt Leu	aaa Lys	gag Glu 785	aac Asn	gat Asp	agc Ser	ctc Leu	2409
ttt Phe 790	tta Leu	agt Ser	gcc Ala	aaa Lys	aaa Lys	gaa Glu 795	aac Asn	aag Lys	ccc Pro	ctg Leu	aaa Lys 800	ttc Phe	agc Ser	ccg Pro	agc Ser	2457
gct Ala 805	tca Ser	aag Lys	gtg Val	ttt Phe	gac Asp 810	gct Ala	agc Ser	aga Arg	gag Glu 815	gtt Val	tat Tyr	cgc Arg	tat Tyr	tac Tyr	cac His 820	2505
aca	caa	gat	ttc	aca	aac	cgc	ccc	tat	aac	gct	aac	gca	agc	ctt	tat	2553







725 730 735  
 Phe His Thr Gln Asn Arg Ile Thr Thr Ala Gln Gly Thr Asn His Phe  
 740 745 750  
 Ile Pro Phe Ser Glu Thr Glu Val Asn Ala Lys Glu Arg Tyr Ser Ser  
 755 760 765  
 His Ala Leu Leu Glu Phe Leu Lys Gly Glu Ile Lys Glu Leu Lys Glu  
 770 775 780  
 Asn Asp Ser Leu Phe Leu Ser Ala Lys Lys Glu Asn Lys Pro Leu Lys  
 785 790 795 800  
 Phe Ser Pro Ser Ala Ser Lys Val Phe Asp Ala Ser Arg Glu Val Tyr  
 805 810 815  
 Arg Tyr Tyr His Thr Gln Asp Phe Thr Asn Arg Pro Tyr Asn Ala Asn  
 820 825 830  
 Ala Ser Leu Tyr Asp Ile Lys Glu Phe Phe Gln Gly Arg Asn Lys Gln  
 835 840 845  
 Gly Lys Leu Asn Leu Pro Ala Lys Ala Lys Asp Glu Tyr Tyr Lys Gln  
 850 855 860  
 Leu Tyr Ala Asn Leu Gln Asp Ala Leu Lys Asp Leu Ala Lys Glu Ile  
 865 870 875 880  
 Gln Pro Lys Val Tyr Glu Tyr Gly Phe Leu Arg Glu  
 885 890

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 <212> DNA  
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<220>  
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 Met Leu Glu Phe Ile Leu Lys Ile Gln Ala Arg Asp Ser Lys  
 1 5 10  
 ggc ttg gtg agc acg att agc acc act atc gct aac aag ggc tat aac 159  
 Gly Leu Val Ser Thr Ile Ser Thr Thr Ile Ala Asn Lys Gly Tyr Asn  
 15 20 25 30  
 atc gtc aaa aac gat gaa ttt gtt gat ccc tta aaa cag cgt ttt ttc 207  
 Ile Val Lys Asn Asp Glu Phe Val Asp Pro Leu Lys Gln Arg Phe Phe  
 35 40 45  
 atg cgg tta aaa atc caa aaa gaa atc aag ccc ttg aat act gaa att 255  
 Met Arg Leu Lys Ile Gln Lys Glu Ile Lys Pro Leu Asn Thr Glu Ile  
 50 55 60  
 aaa gag caa gaa gag caa tcc tta aag acc gct ctt ttt aaa gcc cta 303  
 Lys Glu Gln Glu Glu Gln Ser Leu Lys Thr Ala Leu Phe Lys Ala Leu  
 65 70 75  
 gaa aac ttt aac gag tta ttg att gaa gtc att tta acg cat aaa aaa 351  
 Glu Asn Phe Asn Glu Leu Leu Ile Glu Val Ile Leu Thr His Lys Lys  
 80 85 90  
 aac atc att ctg ctc gct act aaa gag agc cat tgc tta ggg gat ttg 399  
 Asn Ile Ile Leu Leu Ala Thr Lys Glu Ser His Cys Leu Gly Asp Leu

95	100	105	110	
ctt tta agg gtg tat ggg ggg gaa ttg aac gct caa att tta ggc gtt				447
Leu Leu Arg Val Tyr Gly Gly Glu Leu Asn Ala Gln Ile Leu Gly Val	115	120	125	
att tcc aac cac gag att tta cgc cct tta gtg gaa aaa ttt gac atc				495
Ile Ser Asn His Glu Ile Leu Arg Pro Leu Val Glu Lys Phe Asp Ile	130	135	140	
cct tat ttt tat gcg cct tgc gac aat caa gtt ttg cat gaa aaa gaa				543
Pro Tyr Phe Tyr Ala Pro Cys Asp Asn Gln Val Leu His Glu Lys Glu	145	150	155	
gtt tta gaa atc att aaa aac ctg gaa tta aag cac aaa gtg agt gca				591
Val Leu Glu Ile Ile Lys Asn Leu Glu Leu Lys His Lys Val Ser Ala	160	165	170	
gac ttg ctc gtt tta gcc aaa tac atg cgc att tta agc cat gat ttt				639
Asp Leu Leu Val Leu Ala Lys Tyr Met Arg Ile Leu Ser His Asp Phe	175	180	185	190
acg aag cgc tat gaa aac cag atc tta aat atc cat cat agt ttc ttg				687
Thr Lys Arg Tyr Glu Asn Gln Ile Leu Asn Ile His His Ser Phe Leu	195	200	205	
ccc gca ttc att ggg gct aat cct tac cag caa gcg ttt gaa agg ggc				735
Pro Ala Phe Ile Gly Ala Asn Pro Tyr Gln Gln Ala Phe Glu Arg Gly	210	215	220	
gtg aaa gtc atc ggg gcc acg gcg cat ttt gtg aat gaa agc ctt gat				783
Val Lys Val Ile Gly Ala Thr Ala His Phe Val Asn Glu Ser Leu Asp	225	230	235	
gct ggg ccg att atc ata caa gac act ctg ccc att aac cac aat tac				831
Ala Gly Pro Ile Ile Ile Gln Asp Thr Leu Pro Ile Asn His Asn Tyr	240	245	250	
agc gtg gaa aaa atg cgc cta gcg ggt aag gat ata gaa aaa ctg gtt				879
Ser Val Glu Lys Met Arg Leu Ala Gly Lys Asp Ile Glu Lys Leu Val	255	260	265	270
tta gct agg gct tta aaa ctc gtt tta gaa gac aga gtc ttt gta cat				927
Leu Ala Arg Ala Leu Lys Leu Val Leu Glu Asp Arg Val Phe Val His	275	280	285	
gaa aat aaa acg gtg gtg ttt tgaatgcttt tagatttcag caacctcaat				978
Glu Asn Lys Thr Val Val Phe	290			
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<210> 202  
 <211> 259  
 <212> PRT  
 <213> Helicobacter pylori

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 Pro Pro Leu Asp Pro Thr Leu Pro Ala Trp Val Tyr Ser Val Ala Leu  
 35 40 45  
 Leu Lys Val Tyr Phe Ser Asp Gly Thr Tyr Lys Glu Gly Tyr Ala Thr  
 50 55 60  
 Leu Leu Lys Asn Gly Arg Tyr Ile Ala Ser Ser Glu Thr Leu Tyr Ser  
 65 70 75 80  
 Asn Gly Leu Tyr Pro Lys Thr Ile Leu Ala Lys Met Gln Asp Ser Ser  
 85 90 95  
 Ala Lys Glu Leu Ile Cys Ile Ala Ser Leu Arg Leu Glu Ala Met Asp  
 100 105 110  
 Arg Asn Gln Gly Leu Ser Leu Leu Lys Thr Ala Asp Phe Arg Asp Asp  
 115 120 125  
 Tyr Cys His Lys Arg Glu Glu Ser Tyr Tyr His Ala Arg Ile Tyr Thr  
 130 135 140  
 Lys Tyr Ala Gln Thr Phe His Ser Asn Pro Tyr Thr Asn Gln Lys Thr  
 145 150 155 160  
 Pro Asn Ser Asp Leu Tyr Tyr Pro Ala Leu Asn Glu Gly Asn Ser Phe  
 165 170 175  
 Ser Ile Gln Ile Met Gly Ile Ser Val Ala Glu Leu Leu Lys Ser Lys  
 180 185 190  
 Lys Phe Leu Ser Leu Asp Val Ser Phe Lys Lys Gly Ser Val Leu Trp  
 195 200 205  
 Gly Gly Arg Pro Tyr Phe Ser Glu Val Gly Glu Phe Met Gly Met Ala  
 210 215 220  
 Ser Ser Thr Leu Glu Asn Gln Glu Ser Leu Val Ile Ile Pro Lys Glu  
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 Lys Ile Val Gln Phe Leu Asn Ala Leu Lys Asn Gln Asn Ile Phe Pro  
 245 250 255  
 Asn Ile Pro

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<220>  
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 <222> (88)...(603)

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 Met Phe Asp Lys Lys Leu Ser Ser Asn  
 1 5  
 gat tgg cat atc caa aaa gtg gaa atg aac cat caa gtc tat gac att 162  
 Asp Trp His Ile Gln Lys Val Glu Met Asn His Gln Val Tyr Asp Ile  
 10 15 20 25

gaa acc atg ctc gct gat agc gct ttt aga gag cat gaa gaa gag caa 210  
 Glu Thr Met Leu Ala Asp Ser Ala Phe Arg Glu His Glu Glu Glu Gln  
                     30                    35                    40

gat tcc tct cta aat acc gct ttg cct gaa gat aaa aca gcg att gaa 258  
 Asp Ser Ser Leu Asn Thr Ala Leu Pro Glu Asp Lys Thr Ala Ile Glu  
                     45                    50                    55

gcc aaa gag caa gag caa aaa gaa aaa aga aaa cgc tgg tat gag ctt 306  
 Ala Lys Glu Gln Glu Gln Lys Glu Lys Arg Lys Arg Trp Tyr Glu Leu  
                     60                    65                    70

ttt aaa aag aaa cca aag ccc aaa agc tct atg gga gag ttt gtg ttt 354  
 Phe Lys Lys Lys Pro Lys Pro Lys Ser Ser Met Gly Glu Phe Val Phe  
                     75                    80                    85

gat caa aaa gaa aat cgt att tat ggc aaa ggc tat tgc aac cgg tat 402  
 Asp Gln Lys Glu Asn Arg Ile Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr  
                     90                    95                    100                    105

ttt gcc agc tat gta tgg cag ggc gat agg cac att ggg att gaa gat 450  
 Phe Ala Ser Tyr Val Trp Gln Gly Asp Arg His Ile Gly Ile Glu Asp  
                     110                    115                    120

agc ggg att tca aga aaa gtg tgt aaa gat gag cat tta atg gcg ttt 498  
 Ser Gly Ile Ser Arg Lys Val Cys Lys Asp Glu His Leu Met Ala Phe  
                     125                    130                    135

gaa ttg gaa ttt atg gag aat ttt aag ggt aat ttt acg gta act aag 546  
 Glu Leu Glu Phe Met Glu Asn Phe Lys Gly Asn Phe Thr Val Thr Lys  
                     140                    145                    150

ggc aag gac acg ctc att tta gac aac caa aaa atg aaa att tat ttg 594  
 Gly Lys Asp Thr Leu Ile Leu Asp Asn Gln Lys Met Lys Ile Tyr Leu  
                     155                    160                    165

aaa acg cct tgagtgggtt ttgtatttca aaacaatcta agatcactaa 643  
 Lys Thr Pro  
 170

attagggatt aaaaagaaat ttttaa 669

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 <211> 172  
 <212> PRT  
 <213> Helicobacter pylori

<400> 204  
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 Glu Met Asn His Gln Val Tyr Asp Ile Glu Thr Met Leu Ala Asp Ser  
                     20                    25                    30  
 Ala Phe Arg Glu His Glu Glu Glu Gln Asp Ser Ser Leu Asn Thr Ala  
                     35                    40                    45  
 Leu Pro Glu Asp Lys Thr Ala Ile Glu Ala Lys Glu Gln Glu Gln Lys  
                     50                    55                    60  
 Glu Lys Arg Lys Arg Trp Tyr Glu Leu Phe Lys Lys Lys Pro Lys Pro  
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[illegible]

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<221> CDS  
<222> (53) ... (235)
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Leu Thr Leu Thr Pro Ile Lys Arg Phe Leu Glu Lys Gly Asn Asn His  
5 10 15

att gct tca tgg ttg ctt gag cat caa ttt aaa aca aat gct acc aga 202  
Ile Ala Ser Trp Leu Glu His Gln Phe Lys Thr Asn Ala Thr Arg  
35 40 45 50

aacctttgac tgaagtgagg ctcattagta ttttg 290

<400> 206

-234-



[illegible][illegible][illegible]

Ala	Asn	Phe	Gln	Phe	Leu	Trp	Lys	Phe	Gly	Val	Arg	Thr	His	Ile	Ala		
			190						195					200			
aaa	cac	aat	agc	cta	gaa	tta	ggg	att	aaa	gtg	cct	acg	atc	aca	cac	678	
Lys	His	Asn	Ser	Leu	Glu	Leu	Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His		
			205					210					215				
cag	ctt	ttc	tct	ctt	acc	aac	gaa	aag	gga	tac	acc	tta	cag	gct	gat	726	
Gln	Leu	Phe	Ser	Leu	Thr	Asn	Glu	Lys	Gly	Tyr	Thr	Leu	Gln	Ala	Asp		
			220				225					230					
gtg	cgt	aga	gtt	tat	gcg	ttt	caa	atc	agt	tac	ttg	agg	gat	ttt		771	
Val	Arg	Arg	Val	Tyr	Ala	Phe	Gln	Ile	Ser	Tyr	Leu	Arg	Asp	Phe			
			235			240					245						
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<210> 208  
 <211> 248  
 <212> PRT  
 <213> Helicobacter pylori

<400> 208																
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Ala	Glu	Glu	Ser	Ala	Ala	Phe	Val	Gly	Val	Asn	Tyr	Gln	Val	Ser	Met	
			20					25					30			
Ile	Gln	Asn	Gln	Thr	Lys	Met	Val	Asn	Asp	Asn	Gly	Leu	Gln	Lys	Pro	
		35					40					45				
Leu	Ile	Lys	Phe	Pro	Pro	Tyr	Ala	Gly	Ala	Gly	Phe	Glu	Val	Gly	Tyr	
	50					55					60					
Lys	Gln	Phe	Phe	Gly	Lys	Lys	Lys	Trp	Phe	Gly	Met	Arg	Tyr	Tyr	Gly	
65				70					75						80	
Phe	Phe	Asp	Tyr	Ala	His	Asn	Arg	Phe	Gly	Val	Met	Lys	Lys	Gly	Ile	
				85					90					95		
Pro	Val	Gly	Asp	Ser	Gly	Phe	Ile	Tyr	Asn	Ser	Phe	Ser	Phe	Gly	Gly	
			100					105					110			
Asn	Thr	Leu	Thr	Glu	Arg	Asp	Ser	Tyr	Gln	Gly	Gln	Tyr	Tyr	Val	Asn	
		115					120					125				
Leu	Phe	Thr	Tyr	Gly	Val	Gly	Leu	Asp	Thr	Leu	Trp	Asn	Phe	Val	Asn	
	130					135					140					
Lys	Glu	Asn	Met	Val	Phe	Gly	Phe	Val	Val	Gly	Ile	Gln	Leu	Ala	Gly	
145				150					155					160		
Asp	Ser	Trp	Ala	Thr	Ser	Ile	Ser	Lys	Glu	Ile	Ala	His	Tyr	Ala	Lys	
				165					170					175		
His	His	Ser	Asn	Ser	Ser	Tyr	Ser	Pro	Ala	Asn	Phe	Gln	Phe	Leu	Trp	
			180					185					190			
Lys	Phe	Gly	Val	Arg	Thr	His	Ile	Ala	Lys	His	Asn	Ser	Leu	Glu	Leu	
		195					200					205				
Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His	Gln	Leu	Phe	Ser	Leu	Thr	Asn	
	210					215					220					
Glu	Lys	Gly	Tyr	Thr	Leu	Gln	Ala	Asp	Val	Arg	Arg	Val	Tyr	Ala	Phe	
225					230					235					240	
Gln	Ile	Ser	Tyr	Leu	Arg	Asp	Phe									
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<210> 209  
 <211> 1354  
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (190)...(1299)

<400> 209

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aagaaaattt atcatgccaa cagcataaaa atccatgaca cgcaaataa aaacagctac 180  
ccttatgtc gtg cgc gct gca acc aat aat ggt ata aaa ggc ttt att ata 231  
Val Arg Ala Ala Thr Asn Asn Gly Ile Lys Gly Phe Ile Ile  
1 5 10

gat gac cct aca ttt gct aat aaa aaa aat acc ctt tcg ttc gcg caa 279  
Asp Asp Pro Thr Phe Ala Asn Lys Lys Asn Thr Leu Ser Phe Ala Gln  
15 20 25 30

gac act ttc act gtg ttt tat caa aaa caa cct tat ttt aca ggc aat 327  
Asp Thr Phe Thr Val Phe Tyr Gln Lys Gln Pro Tyr Phe Thr Gly Asn  
35 40 45

aag gtt aaa att tta aaa cca aaa ttt gct ttc aaa agc cct aaa att 375  
Lys Val Lys Ile Leu Lys Pro Lys Phe Ala Phe Lys Ser Pro Lys Ile  
50 55 60

tta cat tct ata agc gcg att tta caa ttt att tta aaa ccc tta act 423  
Leu His Ser Ile Ser Ala Ile Leu Gln Phe Ile Leu Lys Pro Leu Thr  
65 70 75

tgg ggg cta ggc tct aca aca gaa agc att gcg gag ttt aaa ttt tct 471  
Trp Gly Leu Gly Ser Thr Thr Glu Ser Ile Ala Glu Phe Lys Phe Ser  
80 85 90

cta ccc cta aaa ccc acc gct aac gct caa acc ctt gag gat att gat 519  
Leu Pro Leu Lys Pro Thr Ala Asn Ala Gln Thr Leu Glu Asp Ile Asp  
95 100 105 110

ttt gat ttc atg gaa aaa ttc ata gcc gaa ctt gag cag tgt cgg ctc 567  
Phe Asp Phe Met Glu Lys Phe Ile Ala Glu Leu Glu Gln Cys Arg Leu  
115 120 125

gcc gaa ctt gag cag tgt cgg ctc gcc gaa ctt cag gct tat tta aaa 615  
Ala Glu Leu Glu Gln Cys Arg Leu Ala Glu Leu Gln Ala Tyr Leu Lys  
130 135 140

gct aca ggg cta gaa aac acc acc ctt tct aac gat gaa gaa aac gcc 663  
Ala Thr Gly Leu Glu Asn Thr Thr Leu Ser Asn Asp Glu Glu Asn Ala  
145 150 155

ctt aat gtt ttc aat aat tct ggg ggg ggg ggg ggt aat acc cca tgc 711  
Leu Asn Val Phe Asn Asn Ser Gly Gly Gly Gly Gly Asn Thr Pro Cys  
160 165 170

ggc tta aca tgg caa agc ttt aga tta ggg gat ttg ttt gaa att gaa 759  
Gly Leu Thr Trp Gln Ser Phe Arg Leu Gly Asp Leu Phe Glu Ile Glu  
175 180 185 190

aaa acc tta agc ttt aat aaa gac gct tta acg caa gga gaa gat tat 807







aac cct agt ttg ttt tgc gaa gcg atc aca aaa agc gcg ttt tat aaa Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Lys 35 40 45 50	200
gat gaa atc gct aaa ctc aaa ggc aaa aaa gct aaa gaa att tat gaa Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu 55 60 65	248
act ctg gcg tta aag gat att tta caa gct tct agc gcg ttg atg cct Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro 70 75 80	296
tta tat gaa aaa gac cct aac aat ggc tac att agc cta gaa att gac Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp 85 90 95	344
cct ttt tta gaa gat gat gcc gct aaa agc att gat gaa gcc aag cgg Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala Lys Arg 100 105 110	392
ttg ttc aaa aca tta aac cgc cct aat gtg atg att aaa gtc cca gcg Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala 115 120 125 130	440
agt gaa agc ggg att gaa gtg gtt agc gct tta act caa gcc tct att Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala Ser Ile 135 140 145	488
cct gtt aat gta act tta gtc ttt tcg cct aaa att gcc ggt gaa atc Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile 150 155 160	536
gct caa atc tta gcc aaa gaa gcg caa aaa aga gcg gtc att agc gtg Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile Ser Val 165 170 175	584
ttt gtc tca cga ttt gac aaa gaa ata gac cct tta gtg cca aaa aat Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Lys Asn 180 185 190	632
ttg caa gct caa agc ggg att atc aac gct acc gag tgc tat tat caa Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr Tyr Gln 195 200 205 210	680
att aat cag cat gcc aat aag cta aca agc acc ctt ttt gca tcc aca Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala Ser Thr 215 220 225	728
ggc gtt aaa tcc aat tct tta gct aaa gat tac tac att aaa gcg ctg Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu 230 235 240	776
tgt ttt aaa aac tct atc aat aca gcc cct cta gag gct tta aac gct Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu Asn Ala 245 250 255	824
tat ttg ctt gac cca aac acc gag tgt caa acc cct tta aag act aca Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Thr Thr	872





290 295 300  
Phe Lys Gln Ser Phe Glu Lys Leu Leu Ser Ser Phe  
305 310 315

<210> 215  
<211> 1254  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (55)...(1215)

<400> 215  
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1

ctc aat ttt atg aca aag aag aaa aat aga atg caa gat tgc aaa atg 105  
Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys Met  
5 10 15

gtt tgt aaa aat ttt aat cgt aag gaa tct gtt ttg ata gct caa tct 153  
Val Cys Lys Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln Ser  
20 25 30

tta gat att tct aaa aaa ggt tcg gta att tta ggc gct ctt ttg agt 201  
Leu Asp Ile Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Leu Ser  
35 40 45

tcg tta tgg ctg aca aac ccc tta aat gcc cat gaa aag aat ggc gcg 249  
Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly Ala  
50 55 60 65

ttt gtg ggg att agc ttg gaa gtg ggt agg gcc gat caa aag aca aac 297  
Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr Asn  
70 75 80

gct tat aaa aac ggc gag ttg ttt caa gtg cct ttt ggc gat gtt tcg 345  
Ala Tyr Lys Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val Ser  
85 90 95

gct aat gat gat ggc aaa gtt cct gac ggg cag acc ggt ggc tgt cag 393  
Ala Asn Asp Asp Gly Lys Val Pro Asp Gly Gln Thr Gly Gly Cys Gln  
100 105 110

cca gct tca ggg acg cca gga acg cca ggc tac act aaa gct aac tgc 441  
Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn Cys  
115 120 125

gtg gtc aat tgg act tcg cgc acc atg ctt agc acc aat aaa aac att 489  
Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn Ile  
130 135 140 145

cct ggc cgt aac cag ccg atg tat ggg cta ggc gtg atg aca ggc tat 537  
Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly Tyr  
150 155 160

aag cat ttt atc ggt aaa aaa aga tgg ttt ggg ttg cgc tat tac ggc 585

Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr	Gly		
			165					170					175				
ttt	ttt	gat	tat	ggg	cat	acc	aat	ttc	tct	aac	tcc	aga	gcc	gct	aac		633
Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala	Asn		
		180					185					190					
gct	ata	tcg	cct	ttt	tat	ttg	agc	gat	caa	aaa	gcc	gac	atg	tat	act		681
Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr	Thr		
	195					200					205						
tat	ggg	ttt	ggc	aca	gac	atg	ctt	ttt	aac	att	ata	gat	aag	cct	aaa		729
Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro	Lys		
210				215						220					225		
gcc	acg	gcc	ggg	ttt	ttt	tta	ggc	gtg	aat	ttt	gcg	ggg	aac	act	tg		777
Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr	Trp		
			230					235					240				
act	aat	aat	cgt	gtg	ggg	tat	ttt	aag	gac	ggg	tat	gtt	tat	ggc	gtc		825
Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly	Val		
			245					250					255				
aat	acg	gac	gct	gac	gct	tac	atg	act	aac	gct	gat	ggc	aca	atc	act		873
Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Thr		
		260					265					270					
tgc	ggg	gac	acg	acg	ccg	gcg	agt	tgc	aat	gtg	ggg	att	aac	cct	aat		921
Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro	Asn		
	275					280					285						
agc	gtc	tat	acc	aca	gga	aaa	ttg	aac	gct	aag	gtg	aat	cac	acg	att		969
Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr	Ile		
	290				295					300					305		
ttc	caa	ttt	tta	gtg	aat	gtg	ggc	att	aga	act	aat	att	ttt	gaa	cac		1017
Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu	His		
			310					315						320			
cat	ggc	att	gag	ttt	ggc	atc	aaa	atc	ccc	acg	ctc	cct	aac	tac	ttt		1065
His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr	Phe		
			325					330					335				
ttc	aaa	ggg	tct	act	acc	ata	aga	gcg	aaa	aaa	caa	ggc	ccg	cta	gag		1113
Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu	Glu		
		340					345					350					
aat	ggc	caa	cca	acc	act	atc	acc	gga	gca	gaa	acc	aat	ttc	agc	tta		1161
Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser	Leu		
		355				360					365						
acc	caa	acc	tta	cgc	cgt	cag	tat	tct	atg	tat	ttg	cgc	tat	gtt	tat		1209
Thr	Gln	Thr	Leu	Arg	Arg	Gln	Tyr	Ser	Met	Tyr	Leu	Arg	Tyr	Val	Tyr		
					375				380						385		
act	ttt	taag	ttt	ggg	agg	gtt	ttt	ta	gg	caa	ggc	ctt	aga	gat	gaa		1254
Thr	Phe																

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 <212> PRT  
 <213> Helicobacter pylori

<400> 216

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Met	Val	Cys	Lys	Asn	Phe	Asn	Arg	Lys	Glu	Ser	Val	Leu	Ile	Ala	Gln
			20					25					30		
Ser	Leu	Asp	Ile	Ser	Lys	Lys	Gly	Ser	Val	Ile	Leu	Gly	Ala	Leu	Leu
		35					40					45			
Ser	Ser	Leu	Trp	Leu	Thr	Asn	Pro	Leu	Asn	Ala	His	Glu	Lys	Asn	Gly
	50					55					60				
Ala	Phe	Val	Gly	Ile	Ser	Leu	Glu	Val	Gly	Arg	Ala	Asp	Gln	Lys	Thr
65					70					75					80
Asn	Ala	Tyr	Lys	Asn	Gly	Glu	Leu	Phe	Gln	Val	Pro	Phe	Gly	Asp	Val
				85					90					95	
Ser	Ala	Asn	Asp	Asp	Gly	Lys	Val	Pro	Asp	Gly	Gln	Thr	Gly	Gly	Cys
			100					105						110	
Gln	Pro	Ala	Ser	Gly	Thr	Pro	Gly	Thr	Pro	Gly	Tyr	Thr	Lys	Ala	Asn
		115					120					125			
Cys	Val	Val	Asn	Trp	Thr	Ser	Arg	Thr	Met	Leu	Ser	Thr	Asn	Lys	Asn
	130					135					140				
Ile	Pro	Gly	Arg	Asn	Gln	Pro	Met	Tyr	Gly	Leu	Gly	Val	Met	Thr	Gly
145					150					155					160
Tyr	Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr
				165					170					175	
Gly	Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala
			180					185					190		
Asn	Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr
		195					200					205			
Thr	Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro
	210					215					220				
Lys	Ala	Thr	Ala	Gly	Phe	Phe	Leu	Gly	Val	Asn	Phe	Ala	Gly	Asn	Thr
225					230					235					240
Trp	Thr	Asn	Asn	Arg	Val	Gly	Tyr	Phe	Lys	Asp	Gly	Tyr	Val	Tyr	Gly
				245					250					255	
Val	Asn	Thr	Asp	Ala	Asp	Ala	Tyr	Met	Thr	Asn	Ala	Asp	Gly	Thr	Ile
			260					265					270		
Thr	Cys	Gly	Asp	Thr	Thr	Pro	Ala	Ser	Cys	Asn	Val	Gly	Ile	Asn	Pro
		275					280					285			
Asn	Ser	Val	Tyr	Thr	Thr	Gly	Lys	Leu	Asn	Ala	Lys	Val	Asn	His	Thr
		290				295					300				
Ile	Phe	Gln	Phe	Leu	Val	Asn	Val	Gly	Ile	Arg	Thr	Asn	Ile	Phe	Glu
305					310					315					320
His	His	Gly	Ile	Glu	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Leu	Pro	Asn	Tyr
				325					330					335	
Phe	Phe	Lys	Gly	Ser	Thr	Thr	Ile	Arg	Ala	Lys	Lys	Gln	Gly	Pro	Leu
			340					345					350		
Glu	Asn	Gly	Gln	Pro	Thr	Thr	Ile	Thr	Gly	Ala	Glu	Thr	Asn	Phe	Ser
		355					360					365			
Leu	Thr	Gln	Thr	Leu	Arg	Arg	Gln	Tyr	Ser	Met	Tyr	Leu	Arg	Tyr	Val
	370					375					380				
Tyr	Thr	Phe													
385															

<210> 217  
 <211> 534

<212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (47)...(481)

<400> 217

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 Ile Tyr Pro Tyr Val Leu Val Val His Leu Leu Cys Ala Ile Ile Phe  
 5 10 15

att ggc tac ttg ttt ttt gat ggg gta att ttc cct aat gtg aag aaa 151  
 Ile Gly Tyr Leu Phe Phe Asp Gly Val Ile Phe Pro Asn Val Lys Lys  
 20 25 30 35

atg ttt ggc gaa gag ttt gcc aat aaa gcg aat aca gga atc act caa 199  
 Met Phe Gly Glu Glu Phe Ala Asn Lys Ala Asn Thr Gly Ile Thr Gln  
 40 45 50

aga gcg atc aaa atc atg ccc tta tgc gtt tta ggg ctt gtt tta aca 247  
 Arg Ala Ile Lys Ile Met Pro Leu Cys Val Leu Gly Leu Val Leu Thr  
 55 60 65

ggg ggc atg atg ctt agc caa tac atg ggg ggc gat aaa ggc tgg tgt 295  
 Gly Gly Met Met Leu Ser Gln Tyr Met Gly Gly Asp Lys Gly Trp Cys  
 70 75 80

gaa acc cct ttt caa aag ata ctc atg ctt aaa gtg atc tta gcg tta 343  
 Glu Thr Pro Phe Gln Lys Ile Leu Met Leu Lys Val Ile Leu Ala Leu  
 85 90 95

agc att ttt ctt ttg gtg ctt ttt tct tta tcg tgt aag ttt ttg ggc 391  
 Ser Ile Phe Leu Leu Val Leu Phe Ser Leu Ser Cys Lys Phe Leu Gly  
 100 105 110 115

aag aaa aac cct att ggt aaa tat atc cac cct atc gct cta act ttt 439  
 Lys Lys Asn Pro Ile Gly Lys Tyr Ile His Pro Ile Ala Leu Thr Phe  
 120 125 130

ggc ttt tta atc gcc att tta gcc aaa acg atg tgg ttt gtt 481  
 Gly Phe Leu Ile Ala Ile Leu Ala Lys Thr Met Trp Phe Val  
 135 140 145

taagagcggt tcaacctcaa agaatttaag accactaaga gtgagctagc gct 534

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 <212> PRT  
 <213> Helicobacter pylori

<400> 218

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 1 5 10 15  
 Ile Ile Phe Ile Gly Tyr Leu Phe Phe Asp Gly Val Ile Phe Pro Asn

[illegible]

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<222> (48) ... (584)
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-247-



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                                   Pro Glu
                                   1

ctt ggt gat ttc gca aga att ggg gtt aat atc cac gcc aaa aag gca      104
Leu Gly Asp Phe Ala Arg Ile Gly Val Asn Ile His Ala Lys Lys Ala
      5                      10                      15

ggt ttc aat aat gga ttt ttt aag att aaa aag ttc ttt ttg gat gtg      152
Val Phe Asn Asn Gly Phe Phe Lys Ile Lys Lys Phe Phe Leu Asp Val
      20                      25                      30

gtg gtg ggg gtc gtt ttc gct atc tgg ttt tat gta gtt aaa gat ttc      200
Val Val Gly Val Val Phe Ala Ile Trp Phe Tyr Val Val Lys Asp Phe
      35                      40                      45                      50

acc cgt tgg cgt gtg gtg aat gat gat ttc atc gtt ttc taatttaaga      249
Thr Arg Trp Arg Val Val Asn Asp Asp Phe Ile Val Phe
                        55                      60

tcgtagcgat acaaggaagc aataagtcct agtcataag caa      292

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<210> 222
<211> 63
<212> PRT
<213> Helicobacter pylori

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<400> 222
Pro Glu Leu Gly Asp Phe Ala Arg Ile Gly Val Asn Ile His Ala Lys
 1                      5                      10                      15
Lys Ala Val Phe Asn Asn Gly Phe Phe Lys Ile Lys Lys Phe Phe Leu
      20                      25                      30
Asp Val Val Val Gly Val Val Phe Ala Ile Trp Phe Tyr Val Val Lys
      35                      40                      45
Asp Phe Thr Arg Trp Arg Val Val Asn Asp Asp Phe Ile Val Phe
      50                      55                      60

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<210> 223
<211> 340
<212> DNA
<213> Helicobacter pylori

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<220>
<221> CDS
<222> (51)...(287)

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                                   Met Phe
                                   1

gaa aaa ata cgc aag att tta gcg gat att gaa gat tcg caa aat gaa      104
Glu Lys Ile Arg Lys Ile Leu Ala Asp Ile Glu Asp Ser Gln Asn Glu
      5                      10                      15

att gaa atg ctt tta aaa tta gcg aat ttg agt ttg ggg gat ttt att      152
Ile Glu Met Leu Leu Lys Leu Ala Asn Leu Ser Leu Gly Asp Phe Ile
      20                      25                      30

```

gag att aaa aga ggg agc atg gac atg cca aag ggc gtg aat gaa gcg 200  
 Glu Ile Lys Arg Gly Ser Met Asp Met Pro Lys Gly Val Asn Glu Ala  
 35 40 45 50

ttt ttt acg caa tta agc gaa gaa gtg gag cga ttg aag gag ctt att 248  
 Phe Phe Thr Gln Leu Ser Glu Glu Val Glu Arg Leu Lys Glu Leu Ile  
 55 60 65

aac gct ttg aat aaa atc aaa aaa ggg tta ttg gtg ttt taaatgtgtg 297  
 Asn Ala Leu Asn Lys Ile Lys Lys Gly Leu Leu Val Phe  
 70 75

ggattgtagg ttatataggg gatagcgaga aaaaatccgt tct 340

<210> 224  
 <211> 79  
 <212> PRT  
 <213> Helicobacter pylori

<400> 224  
 Met Phe Glu Lys Ile Arg Lys Ile Leu Ala Asp Ile Glu Asp Ser Gln  
 1 5 10 15  
 Asn Glu Ile Glu Met Leu Leu Lys Leu Ala Asn Leu Ser Leu Gly Asp  
 20 25 30  
 Phe Ile Glu Ile Lys Arg Gly Ser Met Asp Met Pro Lys Gly Val Asn  
 35 40 45  
 Glu Ala Phe Phe Thr Gln Leu Ser Glu Glu Val Glu Arg Leu Lys Glu  
 50 55 60  
 Leu Ile Asn Ala Leu Asn Lys Ile Lys Lys Gly Leu Leu Val Phe  
 65 70 75

<210> 225  
 <211> 3101  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
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 Met  
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atc caa tcc agc ctt tat aga gcc tta aac aaa ggc ttt gat tac caa 104  
 Ile Gln Ser Ser Leu Tyr Arg Ala Leu Asn Lys Gly Phe Asp Tyr Gln  
 5 10 15

ata ctc gct tgt aag gat ttt aaa gaa tcc gag ctc gct aaa gaa gtc 152  
 Ile Leu Ala Cys Lys Asp Phe Lys Glu Ser Glu Leu Ala Lys Glu Val  
 20 25 30

ata agc tat ttt aag cca aat acc aaa gcc att ctt ttc ccg gag ttt 200  
 Ile Ser Tyr Phe Lys Pro Asn Thr Lys Ala Ile Leu Phe Pro Glu Phe  
 35 40 45

agg gct aaa aaa aac gac gat ttg cgt tcg ttt ttt gaa gaa ttt tta 248



Arg	Ala	Lys	Lys	Asn	Asp	Asp	Leu	Arg	Ser	Phe	Phe	Glu	Glu	Phe	Leu		
50					55					60					65		
cag	ctt	tta	ggg	ggt	tta	agg	gag	ttt	tat	caa	gcc	tta	gaa	aac	aag		296
Gln	Leu	Leu	Gly	Gly	Leu	Arg	Glu	Phe	Tyr	Gln	Ala	Leu	Glu	Asn	Lys		
			70					75						80			
caa	gaa	act	atc	atc	att	gcc	ccg	att	agc	gcg	tta	ttg	cac	cct	tta		344
Gln	Glu	Thr	Ile	Ile	Ile	Ala	Pro	Ile	Ser	Ala	Leu	Leu	His	Pro	Leu		
			85					90					95				
cct	aaa	aaa	gaa	ctt	tta	gaa	agc	ttt	aaa	atc	act	ctt	tta	gaa	aaa		392
Pro	Lys	Lys	Glu	Leu	Leu	Glu	Ser	Phe	Lys	Ile	Thr	Leu	Leu	Glu	Lys		
		100					105					110					
tat	aac	ctt	aag	gat	ttg	aaa	gac	aag	ctc	ttt	tat	tat	ggc	tat	gaa		440
Tyr	Asn	Leu	Lys	Asp	Leu	Lys	Asp	Lys	Leu	Phe	Tyr	Tyr	Gly	Tyr	Glu		
	115					120					125						
att	tta	gac	tta	gtg	gaa	gtg	gaa	ggc	gaa	gcg	agc	ttt	agg	ggg	gat		488
Ile	Leu	Asp	Leu	Val	Glu	Val	Glu	Gly	Glu	Ala	Ser	Phe	Arg	Gly	Asp		
130					135					140					145		
att	gtg	gat	att	tat	gcg	cca	aat	tct	aaa	gcg	tat	cgc	ttg	agt	ttt		536
Ile	Val	Asp	Ile	Tyr	Ala	Pro	Asn	Ser	Lys	Ala	Tyr	Arg	Leu	Ser	Phe		
				150					155					160			
ttt	gac	acc	gag	tgt	gag	agc	att	aag	gaa	ttt	gat	ccc	att	act	caa		584
Phe	Asp	Thr	Glu	Cys	Glu	Ser	Ile	Lys	Glu	Phe	Asp	Pro	Ile	Thr	Gln		
			165					170					175				
atg	agc	ctt	aaa	gaa	gat	ttg	tta	gaa	att	gaa	atc	ccc	ccc	acg	ctt		632
Met	Ser	Leu	Lys	Glu	Asp	Leu	Leu	Glu	Ile	Glu	Ile	Pro	Pro	Thr	Leu		
		180					185					190					
ttt	agt	ttg	gac	gaa	tca	tct	tat	aag	gat	cta	aaa	aca	aaa	gtg	gaa		680
Phe	Ser	Leu	Asp	Glu	Ser	Ser	Tyr	Lys	Asp	Leu	Lys	Thr	Lys	Val	Glu		
	195					200					205						
caa	agc	ccc	tta	aat	agc	ttt	tct	aaa	gat	tta	acc	agt	ttt	ggt	ttg		728
Gln	Ser	Pro	Leu	Asn	Ser	Phe	Ser	Lys	Asp	Leu	Thr	Ser	Phe	Gly	Leu		
210					215					220					225		
tggt	ttt	tta	gga	gaa	aaa	gca	caa	gac	tta	cta	atc	ggt	tat	aaa	agc		776
Trp	Phe	Leu	Gly	Glu	Lys	Ala	Gln	Asp	Leu	Leu	Ile	Val	Tyr	Lys	Ser		
			230					235						240			
att	ata	agt	cct	aga	gct	tta	gaa	gaa	att	caa	gaa	tta	gcg	agc	tta		824
Ile	Ile	Ser	Pro	Arg	Ala	Leu	Glu	Glu	Ile	Gln	Glu	Leu	Ala	Ser	Leu		
			245					250					255				
aac	gaa	ttg	gat	tgt	gag	cgt	ttc	aaa	ttt	tta	aag	ggt	tta	gaa	aac		872
Asn	Glu	Leu	Asp	Cys	Glu	Arg	Phe	Lys	Phe	Leu	Lys	Val	Leu	Glu	Asn		
		260					265					270					
gcg	caa	ggc	tat	gaa	gat	tta	gaa	atc	cat	gcg	cat	gcc	cta	gaa	ggc		920
Ala	Gln	Gly	Tyr	Glu	Asp	Leu	Glu	Ile	His	Ala	His	Ala	Leu	Glu	Gly		
	275					280					285						

ttt atc gct ttg cat tca aat cat aaa atc acg ctc cta gcc ccc aat Phe Ile Ala Leu His Ser Asn His Lys Ile Thr Leu Leu Ala Pro Asn 290 295 300 305	968
aaa acg att tta gac aac gcg ata agc gcg ctt gat gca ggc aac atg Lys Thr Ile Leu Asp Asn Ala Ile Ser Ala Leu Asp Ala Gly Asn Met 310 315 320	1016
gaa tgc gtc atc gcc ccc ttt gtg tta aac ttt aaa acc cct gat ggg Glu Cys Val Ile Ala Pro Phe Val Leu Asn Phe Lys Thr Pro Asp Gly 325 330 335	1064
att ttt att tcg ctc aat tct ttt gaa agg aag aaa aaa cgc caa aaa Ile Phe Ile Ser Leu Asn Ser Phe Glu Arg Lys Lys Lys Arg Gln Lys 340 345 350	1112
tcc aag ctc gct ttg aat gag ttg aat ccg ggc gaa tgg gtg gtg cat Ser Lys Leu Ala Leu Asn Glu Leu Asn Pro Gly Glu Trp Val Val His 355 360 365	1160
gat gat tat ggg gtg ggc gtg ttt tct caa tta gtc cag cac agc gtt Asp Asp Tyr Gly Val Gly Val Phe Ser Gln Leu Val Gln His Ser Val 370 375 380 385	1208
tta ggg agc aag agg gat ttt tta gaa atc gct tat ttg ggc gaa gac Leu Gly Ser Lys Arg Asp Phe Leu Glu Ile Ala Tyr Leu Gly Glu Asp 390 395 400	1256
aaa ctg ctg tta ccg gta gaa aac ttg cat ctc atc gct cgc tat gtg Lys Leu Leu Leu Pro Val Glu Asn Leu His Leu Ile Ala Arg Tyr Val 405 410 415	1304
gcg caa agc gat agc gtg cca gct aaa gac cgg cta ggg aaa ggg agc Ala Gln Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly Ser 420 425 430	1352
ttt ctt aaa tta aaa gct aaa gtc agg act aag ctt tta gag att gct Phe Leu Lys Leu Lys Ala Lys Val Arg Thr Lys Leu Leu Glu Ile Ala 435 440 445	1400
agc aag atc att gaa tta gcg gct gaa cgc aat ttg atc ttg ggt aaa Ser Lys Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly Lys 450 455 460 465	1448
aag atg gat gtg cat tta gcg gag ttg gaa gtc ttt aaa tcg cat gcg Lys Met Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His Ala 470 475 480	1496
ggg ttt gaa tac acc agc gat caa gaa aag gct atc gct gaa att tca Gly Phe Glu Tyr Thr Ser Asp Gln Glu Lys Ala Ile Ala Glu Ile Ser 485 490 495	1544
aag gat tta agc tct cac agg gtg atg gat aga tta ttg agt ggg gat Lys Asp Leu Ser Ser His Arg Val Met Asp Arg Leu Leu Ser Gly Asp 500 505 510	1592
gtg ggt ttt ggg aaa aca gaa gtg gcg atg cat gcg att ttt tgc gcg Val Gly Phe Gly Lys Thr Glu Val Ala Met His Ala Ile Phe Cys Ala 515 520 525	1640

ttt ttg aac ggc ttt caa agc gct tta gtt gtg cct acc act tta tta	1688
Phe Leu Asn Gly Phe Gln Ser Ala Leu Val Val Pro Thr Thr Leu Leu	
530 535 540 545	
gcg cac cag cat ttt gag act tta agg gcg cgt ttt gaa aat ttt ggc	1736
Ala His Gln His Phe Glu Thr Leu Arg Ala Arg Phe Glu Asn Phe Gly	
550 555 560	
gtt aaa gtg gct cgt ttg gac agg tat gcg agc gaa aaa aac aag ctt	1784
Val Lys Val Ala Arg Leu Asp Arg Tyr Ala Ser Glu Lys Asn Lys Leu	
565 570 575	
tta aag gcg gtg gaa tta ggg caa gtt gat gcg cta ata ggc acg cat	1832
Leu Lys Ala Val Glu Leu Gly Gln Val Asp Ala Leu Ile Gly Thr His	
580 585 590	
gcg att tta ggc gcg aaa ttc aaa aac ctg ggc ttg gtg gtg gtg gat	1880
Ala Ile Leu Gly Ala Lys Phe Lys Asn Leu Gly Leu Val Val Val Asp	
595 600 605	
gaa gag cat aaa ttt ggc gtg aaa caa aaa gaa gct tta aaa gaa ttg	1928
Glu Glu His Lys Phe Gly Val Lys Gln Lys Glu Ala Leu Lys Glu Leu	
610 615 620 625	
agt aag agc gtg cat ttt tta agc atg tcc gct acg cct atc ccg cgc	1976
Ser Lys Ser Val His Phe Leu Ser Met Ser Ala Thr Pro Ile Pro Arg	
630 635 640	
act cta aac atg gcg ctc tct caa att aag gcg att agt tct tta aaa	2024
Thr Leu Asn Met Ala Leu Ser Gln Ile Lys Gly Ile Ser Ser Leu Lys	
645 650 655	
acc ccg ccc aca gac aga aag ccc agc cgc act ttt ttg aaa gaa aag	2072
Thr Pro Pro Thr Asp Arg Lys Pro Ser Arg Thr Phe Leu Lys Glu Lys	
660 665 670	
aat gac gaa ctc tta aaa gag att att tac aga gaa tta cgc cgt aac	2120
Asn Asp Glu Leu Leu Lys Glu Ile Ile Tyr Arg Glu Leu Arg Arg Asn	
675 680 685	
ggg caa att ttt tac atc cat aac cac atc gct agc att tta aaa gtc	2168
Gly Gln Ile Phe Tyr Ile His Asn His Ile Ala Ser Ile Leu Lys Val	
690 695 700 705	
aaa acc aag cta gaa gat tta atc cct aaa ctc aaa atc gct att ttg	2216
Lys Thr Lys Leu Glu Asp Leu Ile Pro Lys Leu Lys Ile Ala Ile Leu	
710 715 720	
cat tcc cag att aac gct aat gag agc gaa gaa atc atg cta gag ttt	2264
His Ser Gln Ile Asn Ala Asn Glu Ser Glu Glu Ile Met Leu Glu Phe	
725 730 735	
gcc aag gga aat tat cag gtt tta tta tgc act tct att gtg gaa tca	2312
Ala Lys Gly Asn Tyr Gln Val Leu Leu Cys Thr Ser Ile Val Glu Ser	
740 745 750	
ggg att cat ttg cct aac gct aac acg atc att ata gat aat gcg caa	2360
Gly Ile His Leu Pro Asn Ala Asn Thr Ile Ile Ile Asp Asn Ala Gln	



Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 ± 2.0
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	30 (60.0%)
Unemployed	20 (40.0%)
Income (USD/month)	1000.0 ± 500.0
Health status	
Good	30 (60.0%)
Poor	20 (40.0%)
Comorbidities	
Hypertension	15 (30.0%)
Diabetes	10 (20.0%)
Cholesterol	12 (24.0%)
Arthritis	8 (16.0%)
Other	5 (10.0%)

3101

```
<210> 226
<211> 999
<212> PRT
<213> Helicobacter pylori
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	<400> 226														
Met 1	Ile	Gln	Ser	Ser 5	Leu	Tyr	Arg	Ala	Leu 10	Asn	Lys	Gly	Phe	Asp 15	Tyr
Gln	Ile	Leu	Ala 20	Cys	Lys	Asp	Phe	Lys 25	Glu	Ser	Glu	Leu	Ala 30	Lys	Glu
Val	Ile	Ser 35	Tyr	Phe	Lys	Pro	Asn 40	Thr	Lys	Ala	Ile	Leu 45	Phe	Pro	Glu
Phe	Arg 50	Ala	Lys	Lys	Asn	Asp 55	Leu	Arg	Ser	Phe 60	Glu	Glu	Phe		
Leu 65	Gln	Leu	Leu	Gly 70	Gly	Leu	Arg	Glu	Phe 75	Tyr	Gln	Ala	Leu	Glu	Asn 80
Lys	Gln	Glu	Thr	Ile 85	Ile	Ile	Ala	Pro	Ile 90	Ser	Ala	Leu	Leu	His 95	Pro
Leu	Pro	Lys	Lys 100	Glu	Leu	Leu	Glu	Ser 105	Phe	Lys	Ile	Thr	Leu 110	Leu	Glu
Lys	Tyr	Asn 115	Leu	Lys	Asp	Leu	Lys 120	Asp	Lys	Leu	Phe	Tyr 125	Tyr	Gly	Tyr
Glu	Ile 130	Leu	Asp	Leu	Val	Glu 135	Val	Glu	Gly	Glu	Ala 140	Ser	Phe	Arg	Gly
Asp 145	Ile	Val	Asp	Ile 150	Tyr	Ala	Pro	Asn	Ser	Lys 155	Ala	Tyr	Arg	Leu	Ser 160
Phe	Phe	Asp	Thr	Glu 165	Cys	Glu	Ser	Ile	Lys 170	Glu	Phe	Asp	Pro	Ile 175	Thr
Gln	Met	Ser	Leu 180	Lys	Glu	Asp	Leu	Leu 185	Glu	Ile	Glu	Ile	Pro 190	Pro	Thr
Leu	Phe	Ser 195	Leu	Asp	Glu	Ser	Ser 200	Tyr	Lys	Asp	Leu	Lys 205	Thr	Lys	Val
Glu	Gln 210	Ser	Pro	Leu	Asn	Ser 215	Phe	Ser	Lys	Asp	Leu	Thr 220	Ser	Phe	Gly
Leu 225	Trp	Phe	Leu	Gly 230	Glu	Lys	Ala	Gln	Asp	Leu 235	Leu	Ile	Val	Tyr	Lys 240
Ser	Ile	Ile	Ser	Pro 245	Arg	Ala	Leu	Glu	Glu 250	Ile	Gln	Glu	Leu	Ala 255	Ser
Leu	Asn	Glu	Leu 260	Asp	Cys	Glu	Arg	Phe 265	Lys	Phe	Leu	Lys 270	Val	Leu	Glu
Asn	Ala	Gln 275	Gly	Tyr	Glu	Asp	Leu 280	Glu	Ile	His	Ala	His 285	Ala	Leu	Glu
Gly	Phe 290	Ile	Ala	Leu	His	Ser 295	Asn	His	Lys	Ile	Thr 300	Leu	Leu	Ala	Pro
Asn 305	Lys	Thr	Ile	Leu	Asp 310	Asn	Ala	Ile	Ser	Ala 315	Leu	Asp	Ala	Gly	Asn 320
Met	Glu	Cys	Val	Ile 325	Ala	Pro	Phe	Val	Leu 330	Asn	Phe	Lys	Thr	Pro	Asp
Gly	Ile	Phe	Ile 340	Ser	Leu	Asn	Ser	Phe 345	Glu	Arg	Lys	Lys	Lys 350	Arg	Gln
Lys	Ser	Lys 355	Leu	Ala	Leu	Asn	Glu 360	Leu	Asn	Pro	Gly	Glu 365	Trp	Val	Val
His	Asp 370	Asp	Tyr	Gly	Val	Gly 375	Val	Phe	Ser	Gln	Leu	Val 380	Gln	His	Ser

Val	Leu	Gly	Ser	Lys	Arg	Asp	Phe	Leu	Glu	Ile	Ala	Tyr	Leu	Gly	Glu
385					390					395					400
Asp	Lys	Leu	Leu	Leu	Pro	Val	Glu	Asn	Leu	His	Leu	Ile	Ala	Arg	Tyr
				405					410					415	
Val	Ala	Gln	Ser	Asp	Ser	Val	Pro	Ala	Lys	Asp	Arg	Leu	Gly	Lys	Gly
			420					425					430		
Ser	Phe	Leu	Lys	Leu	Lys	Ala	Lys	Val	Arg	Thr	Lys	Leu	Leu	Glu	Ile
		435					440					445			
Ala	Ser	Lys	Ile	Ile	Glu	Leu	Ala	Ala	Glu	Arg	Asn	Leu	Ile	Leu	Gly
	450					455					460				
Lys	Lys	Met	Asp	Val	His	Leu	Ala	Glu	Leu	Glu	Val	Phe	Lys	Ser	His
465					470					475					480
Ala	Gly	Phe	Glu	Tyr	Thr	Ser	Asp	Gln	Glu	Lys	Ala	Ile	Ala	Glu	Ile
				485					490					495	
Ser	Lys	Asp	Leu	Ser	Ser	His	Arg	Val	Met	Asp	Arg	Leu	Leu	Ser	Gly
			500					505					510		
Asp	Val	Gly	Phe	Gly	Lys	Thr	Glu	Val	Ala	Met	His	Ala	Ile	Phe	Cys
		515					520					525			
Ala	Phe	Leu	Asn	Gly	Phe	Gln	Ser	Ala	Leu	Val	Val	Pro	Thr	Thr	Leu
	530					535					540				
Leu	Ala	His	Gln	His	Phe	Glu	Thr	Leu	Arg	Ala	Arg	Phe	Glu	Asn	Phe
545					550					555					560
Gly	Val	Lys	Val	Ala	Arg	Leu	Asp	Arg	Tyr	Ala	Ser	Glu	Lys	Asn	Lys
				565					570					575	
Leu	Leu	Lys	Ala	Val	Glu	Leu	Gly	Gln	Val	Asp	Ala	Leu	Ile	Gly	Thr
			580					585					590		
His	Ala	Ile	Leu	Gly	Ala	Lys	Phe	Lys	Asn	Leu	Gly	Leu	Val	Val	Val
		595					600					605			
Asp	Glu	Glu	His	Lys	Phe	Gly	Val	Lys	Gln	Lys	Glu	Ala	Leu	Lys	Glu
	610					615					620				
Leu	Ser	Lys	Ser	Val	His	Phe	Leu	Ser	Met	Ser	Ala	Thr	Pro	Ile	Pro
625					630					635					640
Arg	Thr	Leu	Asn	Met	Ala	Leu	Ser	Gln	Ile	Lys	Gly	Ile	Ser	Ser	Leu
				645					650					655	
Lys	Thr	Pro	Pro	Thr	Asp	Arg	Lys	Pro	Ser	Arg	Thr	Phe	Leu	Lys	Glu
			660					665					670		
Lys	Asn	Asp	Glu	Leu	Leu	Lys	Glu	Ile	Ile	Tyr	Arg	Glu	Leu	Arg	Arg
		675					680					685			
Asn	Gly	Gln	Ile	Phe	Tyr	Ile	His	Asn	His	Ile	Ala	Ser	Ile	Leu	Lys
	690					695					700				
Val	Lys	Thr	Lys	Leu	Glu	Asp	Leu	Ile	Pro	Lys	Leu	Lys	Ile	Ala	Ile
705					710					715					720
Leu	His	Ser	Gln	Ile	Asn	Ala	Asn	Glu	Ser	Glu	Glu	Ile	Met	Leu	Glu
				725					730					735	
Phe	Ala	Lys	Gly	Asn	Tyr	Gln	Val	Leu	Cys	Thr	Ser	Ile	Val	Glu	
			740					745					750		
Ser	Gly	Ile	His	Leu	Pro	Asn	Ala	Asn	Thr	Ile	Ile	Ile	Asp	Asn	Ala
		755					760					765			
Gln	Asn	Phe	Gly	Leu	Ala	Asp	Leu	His	Gln	Leu	Arg	Gly	Arg	Val	Gly
	770					775					780				
Arg	Gly	Lys	Lys	Glu	Gly	Phe	Cys	Tyr	Phe	Leu	Ile	Glu	Asp	Gln	Lys
785					790					795					800
Ser	Leu	Asn	Glu	Gln	Ala	Leu	Lys	Arg	Leu	Leu	Ala	Leu	Glu	Lys	Asn
				805					810					815	
Ser	Tyr	Leu	Gly	Ser	Gly	Glu	Ser	Val	Ala	Tyr	His	Asp	Leu	Glu	Ile
		820						825					830		
Arg	Gly	Gly	Gly	Asn	Leu	Leu	Gly	Gln	Asp	Gln	Ser	Gly	His	Ile	Lys
		835					840					845			
Asn	Ile	Gly	Tyr	Ala	Leu	Tyr	Thr	Arg	Met	Leu	Glu	Asp	Ala	Ile	Tyr

850		855		860
Glu Leu Ser Gly Gly Lys Lys Arg Leu Glu Lys Ser Val Glu Ile Gln				
865		870		875
Leu Gly Val Ser Ala Phe Leu Asn Pro Glu Leu Ile Ala Ser Asp Ser				
	885		890	895
Leu Arg Leu Asp Leu Tyr Arg Arg Leu Ser Leu Cys Glu Asn Thr Asp				
	900		905	910
Glu Val Gly Gln Ile His Glu Glu Ile Glu Asp Arg Phe Gly Lys Ile				
	915		920	925
Asp Asp Leu Ser Ala Gln Phe Leu Gln Ile Ile Thr Leu Lys Ile Leu				
	930		935	940
Ala Asn Gln Leu Gly Ile Ile Lys Leu Ser Asn Phe Asn Gln Asn Ile				
	945		950	955
Thr Ile Thr Tyr Ser Asp Glu Lys Lys Glu Ser Leu Lys Ala Pro Ser				
	965		970	975
Lys Asp Asp Asn Asp Ile Leu Glu Thr Leu Leu Lys His Leu Arg Ala				
	980		985	990
Gln Ile Ser Leu Lys Arg Arg				
	995			

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (46)...(1161)

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Met Gln His Glu	
1	
atc cct att gcc ttt gcc ttt gat aaa aac tac cta aaa aca ggg gct	105
Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu Lys Thr Gly Ala	
5 10 15 20	
gtg gct ctc tac tct tta ttg cat gcc cat cgt gca gtt gaa ggg gta	153
Val Ala Leu Tyr Ser Leu Leu His Ala His Arg Ala Val Glu Gly Val	
25 30 35	
ttt ttc agt atc tat ata ttc tat agc ggt ttg aat gaa gat gat tta	201
Phe Phe Ser Ile Tyr Ile Phe Tyr Ser Gly Leu Asn Glu Asp Asp Leu	
40 45 50	
aac agg ctc caa gaa act atc aaa cct ttc aaa cat ttt gcc gct tta	249
Asn Arg Leu Gln Glu Thr Ile Lys Pro Phe Lys His Phe Ala Ala Leu	
55 60 65	
aaa tgc caa gat att agc gcc act ctt gat tct ttg ccc acc atc acg	297
Lys Cys Gln Asp Ile Ser Ala Thr Leu Asp Ser Leu Pro Thr Ile Thr	
70 75 80	
gat agt gca tgg gtt aat cgc tat tct aga atg att ttg gtc aaa tac	345
Asp Ser Ala Trp Val Asn Arg Tyr Ser Arg Met Ile Leu Val Lys Tyr	
85 90 95 100	
ctt ctc cct agt tta ttc ccc caa tac agc aaa atg att tgg tct gat	393

Leu	Leu	Pro	Ser	Leu	Phe	Pro	Gln	Tyr	Ser	Lys	Met	Ile	Trp	Ser	Asp	
				105					110					115		
gtg	gat	gtg	gtc	ttt	tgc	aga	gct	ttc	gct	gat	gat	ttt	atc	gct	tta	441
Val	Asp	Val	Val	Phe	Cys	Arg	Ala	Phe	Ala	Asp	Asp	Phe	Ile	Ala	Leu	
			120					125					130			
gac	aca	agc	gaa	tct	ttt	cat	ttg	agt	ggg	gtg	ata	agt	tta	gta	tca	489
Asp	Thr	Ser	Glu	Ser	Phe	His	Leu	Ser	Gly	Val	Ile	Ser	Leu	Val	Ser	
		135					140					145				
caa	tca	gtt	aca	gag	ggg	ttt	tgg	ttt	tgc	aat	ttg	gat	tac	atg	cga	537
Gln	Ser	Val	Thr	Glu	Gly	Phe	Trp	Phe	Cys	Asn	Leu	Asp	Tyr	Met	Arg	
	150					155					160					
aag	cac	tct	ttc	acc	caa	cag	gtc	tta	gaa	aaa	ttt	aaa	att	caa	gta	585
Lys	His	Ser	Phe	Thr	Gln	Gln	Val	Leu	Glu	Lys	Phe	Lys	Ile	Gln	Val	
165					170					175					180	
atg	cgt	cca	tat	ttt	aaa	gaa	cct	aca	tta	ata	cac	cat	ttg	cat	gct	633
Met	Arg	Pro	Tyr	Phe	Lys	Glu	Pro	Thr	Leu	Ile	His	His	Leu	His	Ala	
				185					190						195	
tat	att	aaa	gaa	ctt	ccc	tta	cac	tat	tgc	gtt	ctg	cct	tat	tat	tat	681
Tyr	Ile	Lys	Glu	Leu	Pro	Leu	His	Tyr	Cys	Val	Leu	Pro	Tyr	Tyr	Tyr	
			200					205					210			
caa	gaa	gaa	ctt	gat	gat	ttg	aga	cat	aaa	gct	tcc	tta	ccc	att	cgg	729
Gln	Glu	Glu	Leu	Asp	Asp	Leu	Arg	His	Lys	Ala	Ser	Leu	Pro	Ile	Arg	
		215					220					225				
ttt	gaa	atc	atc	cac	caa	gac	aaa	ccc	aat	gaa	ttt	atc	cat	cgc	cag	777
Phe	Glu	Ile	Ile	His	Gln	Asp	Lys	Pro	Asn	Glu	Phe	Ile	His	Arg	Gln	
	230					235					240					
caa	atc	ccc	tat	gag	atc	tct	caa	att	caa	aac	att	ctt	tca	aac	cct	825
Gln	Ile	Pro	Tyr	Glu	Ile	Ser	Gln	Ile	Gln	Asn	Ile	Leu	Ser	Asn	Pro	
245					250					255					260	
att	atc	atg	cac	tat	gaa	tct	gat	aaa	gat	gct	ctt	gga	atc	tac	aat	873
Ile	Ile	Met	His	Tyr	Glu	Ser	Asp	Lys	Asp	Ala	Leu	Gly	Ile	Tyr	Asn	
				265					270					275		
ggc	aaa	cct	tgg	gag	ttc	cct	ttg	ggg	aat	caa	tac	cac	ctg	tgg	tta	921
Gly	Lys	Pro	Trp	Glu	Phe	Pro	Leu	Gly	Asn	Gln	Tyr	His	Leu	Trp	Leu	
			280					285					290			
gag	atg	ctt	gca	cac	act	cca	ttt	tgg	aaa	gac	ttc	act	ctg	gaa	atg	969
Glu	Met	Leu	Ala	His	Thr	Pro	Phe	Trp	Lys	Asp	Phe	Thr	Leu	Glu	Met	
		295					300					305				
caa	aaa	aaa	cgc	ata	gaa	tac	cga	gat	att	gct	caa	aaa	atc	cat	tat	1017
Gln	Lys	Lys	Arg	Ile	Glu	Tyr	Arg	Asp	Ile	Ala	Gln	Lys	Ile	His	Tyr	
	310					315					320					
ttt	tct	caa	gat	aag	cgt	ctt	tat	gaa	gtg	agc	ata	cgc	tcc	att	aag	1065
Phe	Ser	Gln	Asp	Lys	Arg	Leu	Tyr	Glu	Val	Ser	Ile	Arg	Ser	Ile	Lys	
325					330					335					340	





340 345 350  
 Glu Arg Trp Ser Lys Pro Ile Lys Thr Phe Phe Gln Lys Asn Phe Phe  
 355 360 365  
 Gln Lys Lys Phe  
 370

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 <212> DNA  
 <213> Helicobacter pylori  
  
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 <221> CDS  
 <222> (250)...(729)

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 taaagagtga aagcggtttt aggagcgta gagtttcaag agaatgaata tgaagagctt 120  
 aaagagcttt atgagagctt aaaaaccaag caaaagcccc acactttgtt catttcttgt 180  
 gtggattcac gagtcgtgcc taattttaatc actggcacca aaccgggcga attgtatgtg 240  
 atttgcaac atg ggc aat gtg aac ccc cct aaa aca agc tat aaa gag tcc 291  
 Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser  
 1 5 10  
  
 ctt tct acc att gcg agc att gaa tac gct atc gcg cat gtg ggc gtt 339  
 Leu Ser Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val  
 15 20 25 30  
  
 caa aac tta atc att tgc ggg cat agc gat tgt ggg gct tgc ggg agc 387  
 Gln Asn Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser  
 35 40 45  
  
 gtt cat tta atc cat gat gaa acc acc aaa gct aaa acc cct tac att 435  
 Val His Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile  
 50 55 60  
  
 gca aac tgg ata caa ttt tta gag cct gtt aaa gaa gag tta aaa aac 483  
 Ala Asn Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn  
 65 70 75  
  
 cac ccg caa ttc agc aac cat ttc gcc aag cgt tca tgg ctt aca gag 531  
 His Pro Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu  
 80 85 90  
  
 cgt ttg aat gcg cgc ttg caa ctc aac aac ctc tta agc tat gat ttc 579  
 Arg Leu Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe  
 95 100 105 110  
  
 att caa gag aaa gcg agc aag aat gaa tta aaa att ttt ggt tgg cac 627  
 Ile Gln Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His  
 115 120 125  
  
 tac atc ata gaa aca ggc agg att tat aat tat aat ttt gaa agc cat 675  
 Tyr Ile Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His  
 130 135 140  
  
 ttt ttt gag ccg att gga gaa acc att aaa caa agg aaa agt cat gaa 723  
 Phe Phe Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu  
 145 150 155

aac ttc taaaacaaaa acccctaaat ccgttttaat cgctgggccca tgcgtcattg 779  
 Asn Phe  
 160

a 780

<210> 230  
 <211> 160  
 <212> PRT  
 <213> Helicobacter pylori

<400> 230  
 Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser Leu Ser  
 1 5 10 15  
 Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val Gln Asn  
 20 25 30  
 Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser Val His  
 35 40 45  
 Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile Ala Asn  
 50 55 60  
 Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn His Pro  
 65 70 75 80  
 Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu Arg Leu  
 85 90 95  
 Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe Ile Gln  
 100 105 110  
 Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His Tyr Ile  
 115 120 125  
 Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His Phe Phe  
 130 135 140  
 Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu Asn Phe  
 145 150 155 160

<210> 231  
 <211> 450  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (107)...(385)

<400> 231  
 taaagataaa aaccacccct tttgaccccc ttttagagga tttttatggt ttttttgaga 60  
 taataaagac ttataaagtt aattaaaatt aaacagaagg gttttg atg tcc gct 115  
 Met Ser Ala  
 1

cat ttt tta aaa atc gtt ttt tta gta ggc atg tgc gtt tca agt ttg 163  
 His Phe Leu Lys Ile Val Phe Leu Val Gly Met Cys Val Ser Ser Leu  
 5 10 15

ttc gct gaa ggt tta gag ggg ttt ttt aac gcc cta gaa gcc cag ctc 211  
 Phe Ala Glu Gly Leu Glu Gly Phe Phe Asn Ala Leu Glu Ala Gln Leu  
 20 25 30 35

aaa agc ccc atc gct aag ggg att tta atg gtg att ttc ata ggg atc 259  
 Lys Ser Pro Ile Ala Lys Gly Ile Leu Met Val Ile Phe Ile Gly Ile



Ala Phe Trp Arg Glu Phe Gly Ile Leu Arg Gln Lys Leu Asn Gly Cys	45	50	55	60	
tgc gcg agc ggt ctt tat gag gct aag ctc gct ttt gaa gaa ttt ggg					304
Cys Ala Ser Gly Leu Tyr Glu Ala Lys Leu Ala Phe Glu Glu Phe Gly	65	70	75		
ggg cga gag agc cac aaa gaa att tgc gtt tat agc ccg gct ttc aaa					352
Gly Arg Glu Ser His Lys Glu Ile Cys Val Tyr Ser Pro Ala Phe Lys	80	85	90		
gag gct gaa atg agc gcg att tta ccc cta gcg aca agc att att ttt					400
Glu Ala Glu Met Ser Ala Ile Leu Pro Leu Ala Thr Ser Ile Ile Phe	95	100	105		
aac tct ttt tac caa tac gct acc tat aaa gac agg att tta gat aaa					448
Asn Ser Phe Tyr Gln Tyr Ala Thr Tyr Lys Asp Arg Ile Leu Asp Lys	110	115	120		
aac aag caa tta gaa aac ttg ggc tta agc ccc att aaa atg ggt ttg					496
Asn Lys Gln Leu Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu	125	130	135	140	
agg ata aac cct ctc tat agc gaa gta acc cca gcg atc tat aac cca					544
Arg Ile Asn Pro Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro	145	150	155		
tgc tct aaa gtg agc cgg tta ggg att acg cct agc gga ttt gaa aag					592
Cys Ser Lys Val Ser Arg Leu Gly Ile Thr Pro Ser Gly Phe Glu Lys	160	165	170		
ggg gtg aaa gag cat ggc tta gag ggg gtg agc ggg ttg cat ttc cat					640
Gly Val Lys Glu His Gly Leu Glu Gly Val Ser Gly Leu His Phe His	175	180	185		
acg cat tgc gag caa aac gct gac gct ttg tgc cgg act tta gag cat					688
Thr His Cys Glu Gln Asn Ala Asp Ala Leu Cys Arg Thr Leu Glu His	190	195	200		
gta gaa aag cat ttc agg ccc tat tta gaa aac atg gcg tgg gtg aat					736
Val Glu Lys His Phe Arg Pro Tyr Leu Glu Asn Met Ala Trp Val Asn	205	210	215	220	
ttt ggt ggg ggg cat cat atc act aag agc gat tat gat gtg aat ttg					784
Phe Gly Gly Gly His His Ile Thr Lys Ser Asp Tyr Asp Val Asn Leu	225	230	235		
ctc atc caa acg att aag gat ttc aaa gaa cgc tat cat aat ata gaa					832
Leu Ile Gln Thr Ile Lys Asp Phe Lys Glu Arg Tyr His Asn Ile Glu	240	245	250		
gtg att tta gag cct ggg gaa gcc ata ggg tgg caa tgc ggg ttt tta					880
Val Ile Leu Glu Pro Gly Glu Ala Ile Gly Trp Gln Cys Gly Phe Leu	255	260	265		
atc gca agc gtg ata gac atc gtt caa aac gat caa gaa att gcg att					928
Ile Ala Ser Val Ile Asp Ile Val Gln Asn Asp Gln Glu Ile Ala Ile	270	275	280		

cta gac gct tct ttt agc gct cac atg ccc gat tgc tta gaa atg cct	976
Leu Asp Ala Ser Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro	
285 290 295 300	
tat cgc cct agc att ttt aaa gtc tcc gta gaa aat gat gaa gag ctt	1024
Tyr Arg Pro Ser Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu	
305 310 315	
att gaa gtt gaa aag ggc gaa aat caa ggg gcg ttt tct tat ttt tta	1072
Ile Glu Val Glu Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu	
320 325 330	
ggc ggc cct act tgt tta gcg ggg gat ttt atg ggg agt ttt agc ttt	1120
Gly Gly Pro Thr Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe	
335 340 345	
gaa acg cct tta aaa agg ggc gat aaa atc gtg ttt caa gac atg ctc	1168
Glu Thr Pro Leu Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu	
350 355 360	
cat tat acg att gtc aaa aac aac tcg ttt aat ggc gtg ccg ctc cca	1216
His Tyr Thr Ile Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro	
365 370 375 380	
agc ctg gct aga ttg gat caa caa ggg ttt aaa atc ctt aaa aac ttt	1264
Ser Leu Ala Arg Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe	
385 390 395	
tct tat gaa gac tat aaa aac aga aac taaagctttt gattaaggct	1311
Ser Tyr Glu Asp Tyr Lys Asn Arg Asn	
400 405	
ttttggggct tgtaaaaaagt tacgcacaac attccaac	1349
<210> 234	
<211> 405	
<212> PRT	
<213> Helicobacter pylori	
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Met Lys Lys Tyr Ser Thr Ile Pro Thr Pro Cys Tyr Val Leu Glu Ser	
1 5 10 15	
Glu Arg Leu Glu Lys Asn Ala Lys Ile Leu Glu Ile Val Arg Gln Gln	
20 25 30	
Ser Gly Ala Lys Val Leu Leu Ala Leu Lys Gly Tyr Ala Phe Trp Arg	
35 40 45	
Glu Phe Gly Ile Leu Arg Gln Lys Leu Asn Gly Cys Cys Ala Ser Gly	
50 55 60	
Leu Tyr Glu Ala Lys Leu Ala Phe Glu Glu Phe Gly Gly Arg Glu Ser	
65 70 75 80	
His Lys Glu Ile Cys Val Tyr Ser Pro Ala Phe Lys Glu Ala Glu Met	
85 90 95	
Ser Ala Ile Leu Pro Leu Ala Thr Ser Ile Ile Phe Asn Ser Phe Tyr	
100 105 110	
Gln Tyr Ala Thr Tyr Lys Asp Arg Ile Leu Asp Lys Asn Lys Gln Leu	
115 120 125	
Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu Arg Ile Asn Pro	
130 135 140	
Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro Cys Ser Lys Val	

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145          150          155          160
Ser Arg Leu Gly Ile Thr Pro Ser Gly Phe Glu Lys Gly Val Lys Glu
165          170          175
His Gly Leu Glu Gly Val Ser Gly Leu His Phe His Thr His Cys Glu
180          185          190
Gln Asn Ala Asp Ala Leu Cys Arg Thr Leu Glu His Val Glu Lys His
195          200          205
Phe Arg Pro Tyr Leu Glu Asn Met Ala Trp Val Asn Phe Gly Gly Gly
210          215          220
His His Ile Thr Lys Ser Asp Tyr Asp Val Asn Leu Leu Ile Gln Thr
225          230          235
Ile Lys Asp Phe Lys Glu Arg Tyr His Asn Ile Glu Val Ile Leu Glu
245          250          255
Pro Gly Glu Ala Ile Gly Trp Gln Cys Gly Phe Leu Ile Ala Ser Val
260          265          270
Ile Asp Ile Val Gln Asn Asp Gln Glu Ile Ala Ile Leu Asp Ala Ser
275          280          285
Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro Tyr Arg Pro Ser
290          295          300
Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu Ile Glu Val Glu
305          310          315
Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu Gly Gly Pro Thr
325          330          335
Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe Glu Thr Pro Leu
340          345          350
Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu His Tyr Thr Ile
355          360          365
Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro Ser Leu Ala Arg
370          375          380
Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe Ser Tyr Glu Asp
385          390          395          400
Tyr Lys Asn Arg Asn
405

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<210> 235  
 <211> 609  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (246)...(548)

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ctcatctttac acttgcaggc tcgcatggcc caaactacga caacaaagtg ccttttaaatt      120
ttaggggtggt taagccttat tgctcaagcg ctgatctgtc ttcttgctcc aaagaaagcc      180
tgattaacgc ctatgacaac accattttttt acaacgacta tctgctagat cgaaagatca      240
ttagc atg ctt gaa aac gcc aag cag ccc gcc tta atg atc tat tta agc      290
Met Leu Glu Asn Ala Lys Gln Pro Ala Leu Met Ile Tyr Leu Ser
1          5          10          15

gat cat ggc gaa agt ttg ggc gaa gaa gcg ttc tat ttg cat ggc att      338
Asp His Gly Glu Ser Leu Gly Glu Glu Ala Phe Tyr Leu His Gly Ile
20          25          30

cct aaa agc atc gcc ccc aaa gaa caa tac gag atc ccc ttt atc gtt      386
Pro Lys Ser Ile Ala Pro Lys Glu Gln Tyr Glu Ile Pro Phe Ile Val
35          40          45

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tat gct aat gag cct ttc aaa gaa aag cat tcc atc att caa acc caa 434  
Tyr Ala Asn Glu Pro Phe Lys Glu Lys His Ser Ile Ile Gln Thr Gln  
50 55 60

acc ccc att aat caa aat gtg att ttc cat agc gtt tta ggg gtg ttt 482  
Thr Pro Ile Asn Gln Asn Val Ile Phe His Ser Val Leu Gly Val Phe  
65 70 75

ttg gat ttt aaa aac cca agc gtt gtt tat cgc cct tct tta gat ctg 530  
Leu Asp Phe Lys Asn Pro Ser Val Val Tyr Arg Pro Ser Leu Asp Leu  
80 85 90 95

ctt aaa cac aaa aaa gag taaaataaca cgcatgaaaa aattcttatt 578  
Leu Lys His Lys Lys Glu  
100

taaacaaaaa ttttgtgaaa gcctgccc aa 609

<210> 236  
<211> 101  
<212> PRT  
<213> Helicobacter pylori

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Met Leu Glu Asn Ala Lys Gln Pro Ala Leu Met Ile Tyr Leu Ser Asp  
1 5 10 15  
His Gly Glu Ser Leu Gly Glu Glu Ala Phe Tyr Leu His Gly Ile Pro  
20 25 30  
Lys Ser Ile Ala Pro Lys Glu Gln Tyr Glu Ile Pro Phe Ile Val Tyr  
35 40 45  
Ala Asn Glu Pro Phe Lys Glu Lys His Ser Ile Ile Gln Thr Gln Thr  
50 55 60  
Pro Ile Asn Gln Asn Val Ile Phe His Ser Val Leu Gly Val Phe Leu  
65 70 75 80  
Asp Phe Lys Asn Pro Ser Val Val Tyr Arg Pro Ser Leu Asp Leu Leu  
85 90 95  
Lys His Lys Lys Glu  
100

<210> 237  
<211> 872  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (123)...(818)

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agtttttagcg ataattatat cttttatggc aataaaaacga gcgtttgtaa gcaaatacggt 60  
aacgctgtgc ctcctcttct agccctagcc ttaggcaaag cgatcttaaa aagcttaaga 120  
aa atg ata caa att tat cac gct gac gct ttt gaa atc atc aaa gac 167  
Met Ile Gln Ile Tyr His Ala Asp Ala Phe Glu Ile Ile Lys Asp  
1 5 10 15

ttt tac cag caa aat tta aaa gtg gat gcg atc atc acg gac cct cct 215  
Phe Tyr Gln Gln Asn Leu Lys Val Asp Ala Ile Ile Thr Asp Pro Pro  
20 25 30



tat aac att tcg gtt aaa aac aat ttt ccc acc cta aag agc gct aaa Tyr Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys 35 40 45	263
agg caa ggc ata gat ttt ggg gaa tgg gat aaa aat ttc aag ctt tta Arg Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu 50 55 60	311
gaa tgg atc gca cgc tac gcc ccc tta gtc aat cca aac ggc tgc atg Glu Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met 65 70 75	359
gtt att ttt tgc tct tac agg ttt ata agc tat atc gct gat ttt tta Val Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu 80 85 90 95	407
gaa gaa aac ggc ttt gtg gtc aaa gac ttt atc caa tgg gtt aaa aat Glu Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn 100 105 110	455
aat ccc atg cca aga aac att cac cgg cgt tat gtc caa gac acg gaa Asn Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu 115 120 125	503
ttt gct ctg tgg gcg gtt aaa aag aaa gcc aag tgg gtg ttt aac aaa Phe Ala Leu Trp Ala Val Lys Lys Lys Ala Lys Trp Val Phe Asn Lys 130 135 140	551
ccc aaa aat gaa aaa tat tta cgg cct ttg att tta aaa agc cct gtg Pro Lys Asn Glu Lys Tyr Leu Arg Pro Leu Ile Leu Lys Ser Pro Val 145 150 155	599
gta agc ggg ctt gaa aaa acc aaa cac ccc acg caa aaa agc ctg gcc Val Ser Gly Leu Glu Lys Thr Lys His Pro Thr Gln Lys Ser Leu Ala 160 165 170 175	647
tta atg gaa aaa atc att tcc atc cac aca aac cct aat gac atc gtg Leu Met Glu Lys Ile Ile Ser Ile His Thr Asn Pro Asn Asp Ile Val 180 185 190	695
cta gat cct ttc atg ggg agc ggc acc acc ggc tta gcg tgc aaa aat Leu Asp Pro Phe Met Gly Ser Gly Thr Thr Gly Leu Ala Cys Lys Asn 195 200 205	743
tta gaa cgg aat ttt atc ggc ata gaa tca gaa aaa gaa tat ttt caa Leu Glu Arg Asn Phe Ile Gly Ile Glu Ser Glu Lys Glu Tyr Phe Gln 210 215 220	791
acc gct aaa aag cgt ttg aat ctg ttt taaaaacgct atttgaatga Thr Ala Lys Lys Arg Leu Asn Leu Phe 225 230	838
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<210> 238

<211> 232

<212> PRT

<213> Helicobacter pylori

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Tyr	Gln	Gln	Asn 20	Leu	Lys	Val	Asp	Ala 25	Ile	Ile	Thr	Asp	Pro 30	Pro	Tyr	
Asn	Ile	Ser 35	Val	Lys	Asn	Asn	Phe 40	Pro	Thr	Leu	Lys	Ser 45	Ala	Lys	Arg	
Gln	Gly 50	Ile	Asp	Phe	Gly	Glu 55	Trp	Asp	Lys	Asn	Phe 60	Lys	Leu	Leu	Glu	
Trp 65	Ile	Ala	Arg	Tyr 70	Ala	Pro	Leu	Val	Asn	Pro 75	Asn	Gly	Cys	Met	Val 80	
Ile	Phe	Cys	Ser 85	Tyr	Arg	Phe	Ile	Ser	Tyr 90	Ile	Ala	Asp	Phe	Leu 95	Glu	
Glu	Asn	Gly 100	Phe	Val	Val	Lys	Asp	Phe 105	Ile	Gln	Trp	Val	Lys 110	Asn	Asn	
Pro	Met	Pro 115	Arg	Asn	Ile	His	Arg	Arg	Tyr	Val	Gln	Asp 125	Thr	Glu	Phe	
Ala	Leu 130	Trp	Ala	Val	Lys	Lys 135	Lys	Ala	Lys	Trp	Val 140	Phe	Asn	Lys	Pro	
Lys 145	Asn	Glu	Lys	Tyr 150	Leu	Arg	Pro	Leu	Ile	Leu 155	Lys	Ser	Pro	Val	Val 160	
Ser	Gly	Leu	Glu 165	Lys	Thr	Lys	His	Pro	Thr 170	Gln	Lys	Ser	Leu	Ala 175	Leu	
Met	Glu	Lys 180	Ile	Ile	Ser	Ile	His	Thr 185	Asn	Pro	Asn	Asp 190	Ile	Val	Leu	
Asp	Pro 195	Phe	Met	Gly	Ser	Gly	Thr 200	Thr	Gly	Leu	Ala	Cys 205	Lys	Asn	Leu	
Glu	Arg 210	Asn	Phe	Ile	Gly	Ile 215	Glu	Ser	Glu	Lys	Glu 220	Tyr	Phe	Gln	Thr	
Ala 225	Lys	Lys	Arg	Leu	Asn 230	Leu	Phe									

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<210> 239
<211> 1181
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (60)...(1124)
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atg	aat	tat	aaa	att	tta	gat	tta	ttt	tgt	ggg	gct	ggg	ggt	ttt	agc		
Met	Asn	Tyr	Lys	Ile	Leu	Asp	Leu	Phe	Cys	Gly	Ala	Gly	Gly	Phe	Ser		
1			5			10			15								
gct	ggg	tta	gag	tgt	tta	gaa	gag	ttt	gac	gct	tta	ata	ggg	cta	gat		155
Ala	Gly	Leu	Glu	Cys	Leu	Glu	Glu	Phe	Asp	Ala	Leu	Ile	Gly	Leu	Asp		
			20			25			30								
tgc	gat	aaa	caa	gcc	cta	atc	act	ttt	gaa	aac	aac	cat	aaa	aac	gcc		203
Cys	Asp	Lys	Gln	Ala	Leu	Ile	Thr	Phe	Glu	Asn	Asn	His	Lys	Asn	Ala		
35			40			45											
ata	ggc	gtt	tgt	ggg	gac	atc	act	caa	acc	gaa	att	aaa	gaa	aaa	gtc		251
Ile	Gly	Val	Cys	Gly	Asp	Ile	Thr	Gln	Thr	Glu	Ile	Lys	Glu	Lys	Val		
50			55			60											

atc Ile 65	aaa Lys	cta Leu	gct Ala	aaa Lys	aaa Lys 70	tta Leu	gaa Glu	atc Ile	aac Asn	atg Met 75	atc Ile	att Ile	ggc Gly	ggg Gly	cct Pro 80	299
cca Pro	tgt Cys	caa Gln	ggc Gly	ttt Phe 85	tct Ser	aat Asn	aaa Lys	ggg Gly	aaa Lys 90	aat Asn	tta Leu	ggg Gly	cta Leu	aaa Lys 95	gac Asp	347
cct Pro	agg Arg	aat Asn	ttt Phe 100	tta Leu	ttc Phe	tta Leu	gaa Glu	tat Tyr 105	ata Ile	gaa Glu	ata Ile	gtc Val	aaa Lys 110	gcc Ala	ata Ile	395
aag Lys	cca Pro	gaa Glu 115	att Ile	ttt Phe	atc Ile	att Ile	gaa Glu 120	aac Asn	gtg Val	aaa Lys	aac Asn	ctc Leu 125	atc Ile	tct Ser	tgc Cys	443
gct Ala 130	aaa Lys	ggc Gly	tat Tyr	ttt Phe	tta Leu	gaa Glu 135	gaa Glu	att Ile	aaa Lys	gaa Glu	agg Arg 140	ttg Leu	aac Asn	gct Ala	tta Leu	491
ggg Gly 145	tat Tyr	caa Gln	ttg Leu	agc Ser 150	tat Tyr	caa Gln	atc Ile	cta Leu	aac Asn 155	gct Ala	aaa Lys	gat Asp	tat Tyr	ggc Gly	gtg Val 160	539
cct Pro	caa Gln	aac Asn	aga Arg	gag Glu 165	aga Arg	gcc Ala	ttt Phe	att Ile	gta Val 170	ggg Gly	gct Ala	agt Ser	cgt Arg	ttc Phe 175	agt Ser	587
ttt Phe	gat Asp	ttc Phe	aat Asn 180	ctt Leu	tta Leu	gag Glu	cct Pro	tct Ser 185	caa Gln	agc Ser	gtg Val	aat Asn 190	gtt Val	caa Gln	gat Asp	635
gcc Ala	ata Ile	agc Ser 195	gat Asp	tta Leu	gcc Ala	tat Tyr 200	ctt Leu	tgt Cys	tct Ser	aat Asn	gag Glu	ggg Gly 205	gcg Ala	ttt Phe	gag Glu	683
agc Ser 210	gat Asp	tat Tyr	tta Leu	aac Asn	cct Pro	atc Ile 215	caa Gln	tca Ser	agc Ser	tat Tyr	caa Gln 220	gct Ala	tta Leu	atg Met	cga Arg	731
aaa Lys 225	gat Asp	agc Ser	cct Pro	aaa Lys 230	tta Leu	tac Tyr	aac Asn	cat His	caa Gln 235	gcc Ala	acc Thr	aac Asn	cac His	tcg Ser	caa Gln 240	779
gcc Ala	gct Ala	tta Leu	gag Glu	aaa Lys 245	tta Leu	aaa Lys	ctc Leu	att Ile	aac Asn 250	aaa Lys	gaa Glu	caa Gln	ggc Gly	aaa Lys 255	gaa Glu	827
tgc Cys	ttg Leu	cct Pro	aaa Lys 260	aac Asn	ttg Leu	cat His	ggc Gly	aaa Lys 265	cag Gln	caa Gln	ttc Phe	aaa Lys 270	agc Ser	aca Thr	tgg Trp	875
ggg Gly	cgc Arg	ctg Leu	aat Asn 275	tgg Trp	aat Asn	aaa Lys	atc Ile 280	agc Ser	ccc Pro	acc Thr	ata Ile	gac Asp 285	aca Thr	cga Arg	ttt Phe	923
gac Asp	act Thr 290	ccc Pro	agc Ser	aat Asn	ggc Gly	acc Thr 295	aac Asn	tcc Ser	cac His	ccc Pro	gaa Glu 300	ttg Leu	cac His	cgc Arg	tct Ser	971



Gly Arg Leu Asn Trp Asn Lys Ile Ser Pro Thr Ile Asp Thr Arg Phe  
 275 280 285  
 Asp Thr Pro Ser Asn Gly Thr Asn Ser His Pro Glu Leu His Arg Ser  
 290 295 300  
 Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr  
 305 310 315 320  
 Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala  
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 340 345 350  
 Leu Arg Lys  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (49)...(1305)

<400> 241

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caa tca atg att gat ttt tta aaa ctt aga gat tat gac att aga aaa	105
Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp Ile Arg Lys	
5 10 15	
aca caa aat gcg cga tgg ata gat caa aaa tgc acc cct gat gtg ttg	153
Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro Asp Val Leu	
20 25 30 35	
tct ctt gtt gct gat tgt att tta gag ttt acg caa tgt aat att gga	201
Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys Asn Ile Gly	
40 45 50	
aaa tca ttt tct att agg gat att tgg gat agc cct tac acc aat gaa	249
Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr Thr Asn Glu	
55 60 65	
aat gtt aaa atg att ttt tct aaa cct gat tta aat tct gac ttt tcc	297
Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser Asp Phe Ser	
70 75 80	
atg cat gaa tac gat aag ttt ttt tct cag cct att aaa tta tta gcc	345
Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys Leu Leu Ala	
85 90 95	
tat agc ggt att tta ttt gaa aca aaa act ggc aat aga aat att tat	393
Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg Asn Ile Tyr	
100 105 110 115	
acc ata caa aac ata gag cta tta gaa tat ctc atg caa aga gaa aca	441
Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln Arg Glu Thr	
120 125 130	

aac gct ttg aaa ttc ctt att tta tat att caa aag gta tta atg gat Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val Leu Met Asp 135 140 145	489
agt ggg att tat cct tta ttt gac aac ttt tta caa aaa caa gac aca Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys Gln Asp Thr 150 155 160	537
gaa agt ttt aag caa cta aaa gat ggt ttc act cat ttt act atc aat Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe Thr Ile Asn 165 170 175	585
aac aca gca atc aat aac gct acg gaa tgt ttt agg att ttt act aaa Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile Phe Thr Lys 180 185 190 195	633
att atc aat cct tta gct ttt tat tat ggt aaa aaa ggc aca aga aaa Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly Thr Arg Lys 200 205 210	681
ggg tat ttg tcc aac act ata att aca aaa gat gag ctt aat tat aat Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu Asn Tyr Asn 215 220 225	729
cgt atc aat tgg cga gat ata gga aaa gat aaa aat acc acc aga caa Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr Thr Arg Gln 230 235 240	777
gaa tac gat ctt ata aac tct aaa agg att gct aat tct aac tat ctt Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser Asn Tyr Leu 245 250 255	825
att tca aaa gct aag aaa gtg gtg aaa cga tat aat gat aga ttt aat Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn 260 265 270 275	873
aat tct ctc tct gaa gta aaa caa gaa aaa gaa gag tcg caa gcc aca Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr 280 285 290	921
caa ata cac cat att ttt ccc atc caa gac ttt ccc att att gct aac Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile Ile Ala Asn 295 300 305	969
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gcc cac cct aat aat caa acc cgc ttg att gat aaa gat ttt caa tat Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr 325 330 335	1065
atc tgc tta tta gct aaa acg acc aca att ctt aat gac act caa ggc Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly 340 345 350 355	1113
gta tat gat tgg aat gat tat att gtt gtg ttg aat atg ggc ctc aaa Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met Gly Leu Lys 360 365 370	1161

aca act atc ttt tct caa gtc aag aac gaa tgg gaa tta tta aaa gta 1209  
 Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val  
 375 380 385

ata gat gct ttt tat ttt gat ttt aac aag agc aaa gat cca agt tgg 1257  
 Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp  
 390 395 400

tca tac ttg cta gat aaa aac gat tta aga gct ttc aag cta aaa ttt 1305  
 Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe  
 405 410 415

taataagttt tattgaaact ggctataaaa acccgcttga cttatcttat cctttt 1361

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 <212> PRT  
 <213> Helicobacter pylori

<400> 242

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			20					25					30		
Asp	Val	Leu	Ser	Leu	Val	Ala	Asp	Cys	Ile	Leu	Glu	Phe	Thr	Gln	Cys
		35					40					45			
Asn	Ile	Gly	Lys	Ser	Phe	Ser	Ile	Arg	Asp	Ile	Trp	Asp	Ser	Pro	Tyr
	50					55					60				
Thr	Asn	Glu	Asn	Val	Lys	Met	Ile	Phe	Ser	Lys	Pro	Asp	Leu	Asn	Ser
	65				70					75				80	
Asp	Phe	Ser	Met	His	Glu	Tyr	Asp	Lys	Phe	Phe	Ser	Gln	Pro	Ile	Lys
				85					90					95	
Leu	Leu	Ala	Tyr	Ser	Gly	Ile	Leu	Phe	Glu	Thr	Lys	Thr	Gly	Asn	Arg
			100					105					110		
Asn	Ile	Tyr	Thr	Ile	Gln	Asn	Ile	Glu	Leu	Leu	Glu	Tyr	Leu	Met	Gln
	115					120						125			
Arg	Glu	Thr	Asn	Ala	Leu	Lys	Phe	Leu	Ile	Leu	Tyr	Ile	Gln	Lys	Val
	130					135					140				
Leu	Met	Asp	Ser	Gly	Ile	Tyr	Pro	Leu	Phe	Asp	Asn	Phe	Leu	Gln	Lys
	145				150					155				160	
Gln	Asp	Thr	Glu	Ser	Phe	Lys	Gln	Leu	Lys	Asp	Gly	Phe	Thr	His	Phe
				165					170					175	
Thr	Ile	Asn	Asn	Thr	Ala	Ile	Asn	Asn	Ala	Thr	Glu	Cys	Phe	Arg	Ile
		180					185						190		
Phe	Thr	Lys	Ile	Ile	Asn	Pro	Leu	Ala	Phe	Tyr	Tyr	Gly	Lys	Lys	Gly
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Thr	Arg	Lys	Gly	Tyr	Leu	Ser	Asn	Thr	Ile	Ile	Thr	Lys	Asp	Glu	Leu
	210				215						220				
Asn	Tyr	Asn	Arg	Ile	Asn	Trp	Arg	Asp	Ile	Gly	Lys	Asp	Lys	Asn	Thr
	225				230					235				240	
Thr	Arg	Gln	Glu	Tyr	Asp	Leu	Ile	Asn	Ser	Lys	Arg	Ile	Ala	Asn	Ser
			245						250					255	
Asn	Tyr	Leu	Ile	Ser	Lys	Ala	Lys	Lys	Val	Val	Lys	Arg	Tyr	Asn	Asp
		260					265						270		
Arg	Phe	Asn	Ser	Leu	Ser	Glu	Val	Lys	Gln	Glu	Lys	Glu	Glu	Ser	
	275					280					285				
Gln	Ala	Thr	Gln	Ile	His	His	Ile	Phe	Pro	Ile	Gln	Asp	Phe	Pro	Ile
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[illegible]

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<222> (90) ... (2558)
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t	a	t	a	t	t	t	c	t	t	a	a	a	g	a	a	161
Tyr	Ile	Ser	Leu	Phe	Ser	Gly	Ala	Gly	Val	Gly	Cys	Tyr	Gly	Leu	Leu	
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g	a	a	g	a	g	g	t	t	g	c	t	t	a	a	a	209
Glu	Glu	Gly	Phe	Glu	Cys	Val	Ala	Thr	Asn	Glu	Ile	Leu	Glu	Lys	Arg	
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Leu	Asn	Ile	Gln	Arg	Ile	Asn	Arg	Lys	Cys	Lys	Leu	Asp	Glu	Ser	Tyr	
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a	t	t	a	a	g	a	a	a	a	a	a	a	a	a	a	305
Ile	Ser	Gly	Asp	Ile	Lys	Lys	Pro	Glu	Thr	Lys	Glu	Lys	Ile	Leu	Lys	
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Gln	Ile	Glu	Phe	Tyr	Ser	Lys	Lys	Phe	Gly	Asn	Asp	Arg	Val	Asp	Leu	
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Val	Val	Ala	Thr	Pro	Pro	Cys	Gln	Gly	Met	Ser	Val	Ala	Asn	His	Lys	
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Lys	Lys	Asn	Asp	Glu	Ile	Lys	Arg	Asn	Ser	Leu	Val	Val	Glu	Ser	Ile	
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cct agt ttt tat aaa aca ggt tgt ata gac aaa aat gat aat ttg cta Pro Ser Phe Tyr Lys Thr Gly Cys Ile Asp Lys Asn Asp Asn Leu Leu 140 145 150	545
gaa ata gga tct atg ata gag caa aat ttg agt ggc gat tat atg ctc Glu Ile Gly Ser Met Ile Glu Gln Asn Leu Ser Gly Asp Tyr Met Leu 155 160 165	593
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aca aga act tta gtg ata ggg gtt tgt aaa gag ttt aaa gat ttt ata Thr Arg Thr Leu Val Ile Gly Val Cys Lys Glu Phe Lys Asp Phe Ile 185 190 195 200	689
agc gcg tta gaa ttt ttt cct gat ttc aaa caa gaa aaa acc tta aaa Ser Ala Leu Glu Phe Phe Pro Asp Phe Lys Gln Glu Lys Thr Leu Lys 205 210 215	737
gaa gtg ata gga tcg tta aaa cca ctt gct tgg ggc gag tat gac aac Glu Val Ile Gly Ser Leu Lys Pro Leu Ala Trp Gly Glu Tyr Asp Asn 220 225 230	785
acg gat ttt tat cat agt ttt aga act tat cca aag cat atg caa gaa Thr Asp Phe Tyr His Ser Phe Arg Thr Tyr Pro Lys His Met Gln Glu 235 240 245	833
tgg att aag gat tta aaa gaa gga caa agc gcg ttt gag aat aca gaa Trp Ile Lys Asp Leu Lys Glu Gly Gln Ser Ala Phe Glu Asn Thr Glu 250 255 260	881
tta aac aaa aaa cct cat aga att gtt ggc agt aag att gtc tta aat Leu Asn Lys Lys Pro His Arg Ile Val Gly Ser Lys Ile Val Leu Asn 265 270 275 280	929
gtt tct aaa aat ggc gat aaa tat aaa aga caa aaa tat cat agc gtt Val Ser Lys Asn Gly Asp Lys Tyr Lys Arg Gln Lys Tyr His Ser Val 285 290 295	977
gcc cct tgc att cat aca aga aac gac caa atg gct agc caa aac acg Ala Pro Cys Ile His Thr Arg Asn Asp Gln Met Ala Ser Gln Asn Thr 300 305 310	1025
atc cac ccc aaa gat gat aga gtg ttt tcc att aga gag ctg atg ctt Ile His Pro Lys Asp Asp Arg Val Phe Ser Ile Arg Glu Leu Met Leu 315 320 325	1073
tta atg aat atc cct agc cgt ttt aag tgg tta gat tta gaa tta caa Leu Met Asn Ile Pro Ser Arg Phe Lys Trp Leu Asp Leu Glu Leu Gln 330 335 340	1121
gaa tta aac gcc ctt aac caa caa gaa aaa gaa aaa atc tcc aaa caa Glu Leu Asn Ala Leu Asn Gln Gln Glu Lys Glu Lys Ile Ser Lys Gln 1169	





2610

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<211> 823
<212> PRT
<213> Helicobacter pylori
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Thr	Asn	Glu 35	Ile	Leu	Glu	Lys	Arg 40	Leu	Asn	Ile	Gln 45	Arg	Ile	Asn	Arg
Lys	Cys 50	Lys	Leu	Asp	Glu	Ser 55	Tyr	Ile	Ser	Gly	Asp 60	Ile	Lys	Lys	Pro
Glu 65	Thr	Lys	Glu	Lys	Ile 70	Leu	Lys	Gln	Ile	Glu 75	Phe	Tyr	Ser	Lys	Lys 80
Phe	Gly	Asn	Asp	Arg 85	Val	Asp	Leu	Val	Val 90	Ala	Thr	Pro	Pro	Cys 95	Gln
Gly	Met	Ser	Val 100	Ala	Asn	His	Lys	Lys 105	Lys	Asn	Asp	Glu	Ile 110	Lys	Arg
Asn	Ser	Leu 115	Val	Val	Glu	Ser	Ile 120	Asp	Leu	Ile	Lys	Gln 125	Ile	Lys	Pro
Arg	Phe 130	Phe	Ile	Leu	Glu	Asn 135	Val	Pro	Ser	Phe	Tyr 140	Lys	Thr	Gly	Cys
Ile 145	Asp	Lys	Asn	Asp	Asn 150	Leu	Leu	Glu	Ile	Gly 155	Ser	Met	Ile	Glu	Gln 160
Asn	Leu	Ser	Gly	Asp 165	Tyr	Met	Leu	Tyr	Asp 170	Glu	Val	Ile	Asn	Phe 175	Lys
Asn	Phe	Gly 180	Ala	Asn	Ser	Ser	Arg	Thr 185	Arg	Thr	Leu	Val 190	Ile	Gly	Val
Cys	Lys	Glu 195	Phe	Lys	Asp	Phe	Ile 200	Ser	Ala	Leu	Glu	Phe 205	Phe	Pro	Asp
Phe	Lys 210	Gln	Glu	Lys	Thr	Leu 215	Lys	Glu	Val	Ile	Gly 220	Ser	Leu	Lys	Pro
Leu 225	Ala	Trp	Gly	Glu	Tyr 230	Asp	Asn	Thr	Asp	Phe 235	Tyr	His	Ser	Phe	Arg 240
Thr	Tyr	Pro	Lys	His 245	Met	Gln	Glu	Trp	Ile 250	Lys	Asp	Leu	Lys	Glu 255	Gly
Gln	Ser	Ala	Phe 260	Glu	Asn	Thr	Glu	Leu 265	Asn	Lys	Lys	Pro	His	Arg	Ile
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Lys	Arg 290	Gln	Lys	Tyr	His	Ser 295	Val	Ala	Pro	Cys	Ile 300	His	Thr	Arg	Asn
Asp 305	Gln	Met	Ala	Ser	Gln 310	Asn	Thr	Ile	His	Pro 315	Lys	Asp	Asp	Arg	Val 320
Phe	Ser	Ile	Arg	Glu 325	Leu	Met	Leu	Leu	Met 330	Asn	Ile	Pro	Ser	Arg 335	Phe
Lys	Trp	Leu	Asp 340	Leu	Glu	Leu	Gln	Glu 345	Leu	Asn	Ala	Leu	Asn	Gln	Gln
Glu	Lys	Glu	Lys 355	Ile	Ser	Lys	Gln	Asn	Glu	Met	Asn	Ile 365	Arg	Gln	Ser
Ile	Gly 370	Glu	Ala	Val	Pro	Thr 375	Ile	Ile	Phe	Lys	Gln 380	Ile	Ala	Ile	Lys
Ile 385	Lys	Asn	Phe	Met	Ser 390	Gln	Thr	His	Leu	Glu 395	Pro	Lys	Glu	Ile	Ile 400
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Lys	Asp	Phe	Leu	Ala	Tyr	Glu	Cys	Gly	Lys	Val	Asp	Leu	Ile	Val	Gly	
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Arg	Leu	Thr	His	Leu	Ala	Gly	Ile	Phe	Leu	Glu	Lys	Ser	Leu	Lys	Leu	
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Ala	Asn	Phe	Thr	Ala	Met	Val	Met	Pro	Lys	Asn	Leu	Leu	Asn	Thr	Lys	
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Glu	Tyr	Ala	Glu	Thr	Arg	Thr	Lys	Leu	Glu	Lys	Lys	Gly	Val	Gly	Ala	
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Ile	Leu	Asp	Phe	Gly	Glu	Leu	Gly	Phe	Lys	Gly	Val	Leu	Val	Glu	Thr	
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Ile	Ala	Ile	Val	Thr	Gln	Lys	Ser	Lys	Glu	Val	Leu	Ala	Arg	Ser	Leu	
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Pro	Leu	Asn	Leu	Ser	Ile	Lys	Gln	Lys	Pro	Ser	Tyr	Ile	Phe	Asp	Lys	
				645					650					655		
Gln	Leu	Pro	Tyr	Trp	Val	Ile	Tyr	Arg	Asn	Ala	Phe	Phe	Asp	Lys	Val	
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Phe	His	Ser	Met	Gln	Phe	Gly	Leu	Phe	Glu	Val	Phe	Arg	Asp	Arg	Gln	
		675					680					685				
Ile	Thr	Asn	Ser	Val	Leu	Val	Lys	Asn	Gly	Ile	Arg	Val	Ile	Lys	Ser	
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Arg	Asn	Ile	Asp	Glu	Asn	Gly	Lys	Ile	Ile	Ser	Ile	Glu	Asn	Tyr	Asp	
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[illegible]

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gaa Glu	gac Asp	acc Thr	gct Ala	tat Tyr	aaa Lys	atg Met	tta Leu	aaa Lys	gct Ala	aac Asn	ccc Pro	act Thr	tta Leu	gcc Ala	ttg Leu	2264
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915 920 925																
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930 935 940 945																
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950 955 960																
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965 970 975																
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995 1000 1005																
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1110 1115 1120																
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1125 1130 1135																
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Arg	Glu	Lys	Met	Arg	Asn	Ala	Pro	Ile	Leu	Glu	Leu	Tyr	Pro	Glu	Met	
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Asp	Gly	Arg	Phe	Glu	Asp	Pro	Asn	Leu	Thr	Pro	Leu	Glu	Val	Phe	Asp	
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Ser	Gln	Lys	Ser	Phe	Thr	Glu	Ile	His	Ala	Leu	Met	Ser	Gln	Thr	Ala	
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Gln	Leu	Phe	Arg	Glu	Arg	Arg	Gly	Asp	Leu	Ile	Gly	Ile	Ser	Ala	Leu	
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Glu	Val	Gly	Lys	Thr	Phe	Ala	Glu	Thr	Asp	Ala	Glu	Val	Ser	Glu	Ala	
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Ile	Asp	Phe	Leu	Glu	Phe	Tyr	Pro	Tyr	Ser	Leu	Arg	Val	Leu	Gln	Glu	
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Ala	Pro	Trp	Asn	Phe	Pro	Val	Gly	Ile	Ser	Val	Gly	Thr	Ile	Ala	Ala	
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 Ala Leu Ala Asp Lys Pro Asn Glu Lys Val Ile Lys Ala Ile Asp Glu  
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 Asn Pro Tyr Leu Met Lys Pro Ser Ile Lys Tyr Gly Thr Lys Lys Gly  
 850 855 860  
 Asp Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met  
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 Glu Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly  
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 Tyr Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu  
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 Tyr Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro  
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 Thr Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys  
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 Ser Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr  
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 Gln Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys  
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 Asn Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp  
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 Lys  
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 <222> (107)...(673)



<212> PRT  
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Gly	Phe	Val	Pro	Leu	Lys	Glu	Gly	Phe	Leu	Lys	Ser	Phe	Lys	Glu	Arg
		35					40					45			
Cys	Asn	Leu	Glu	Phe	Leu	Glu	Asn	Leu	Asp	Leu	Leu	Phe	Leu	Tyr	Asp
50						55					60				
Lys	Pro	Ser	Ala	His	Glu	Ile	Phe	Ser	Leu	Cys	Lys	Glu	Leu	Lys	Asn
65				70						75				80	
Ser	Ile	Trp	Asp	Arg	Lys	Leu	Val	Val	Ala	Leu	Val	Glu	Ala	Leu	Glu
			85						90					95	
Gly	Phe	Lys	Asp	Trp	Asn	Leu	Ser	Leu	Lys	Ile	Glu	Asp	Lys	Arg	Ser
			100					105					110		
Asn	Ser	Leu	Gly	Asn	Gly	Thr	Lys	Lys	Leu	Leu	Thr	Asn	Ala	Asp	Leu
		115					120						125		
Gly	Ser	Asp	Tyr	Lys	Thr	Ile	Val	Ile	Asp	Ser	Met	Lys	Thr	Tyr	His
130						135					140				
Gln	Ser	Gln	Gln	Glu	Lys	Tyr	Lys	Arg	Glu	Arg	Gly	Glu	Thr	Leu	Glu
145					150					155					160
Val	Arg	Pro	Thr	Thr	Pro	Pro	Ser	Tyr	Gly	Gly	Gly	Ser	Ile	Arg	Ile
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Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile Gly	
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Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro Phe	
20 25 30	
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Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile Met	
35 40 45	
ctt tta gcg gta agc cct ggc atg atg agg ggc gat gcg caa gat gtg	252
Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp Val	
50 55 60 65	

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ttt gaa aaa atc cat aac act gaa gat ggg ttt gcc agc aga gac atg Phe Glu Lys Ile His Asn Thr Glu Asp Gly Phe Ala Ser Arg Asp Met 85 90 95	348
cat att gtt gtg ggg gaa aac gct ttt tta gat ttt gcg cct ttc ccg His Ile Val Val Gly Glu Asn Ala Phe Leu Asp Phe Ala Pro Phe Pro 100 105 110	396
tta atc ccc ttt gaa aac gcg cat ttt aag ggc aac acc acg att tct Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile Ser 115 120 125	444
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cga gtg gcg cgc aat gag ttg ttt aaa ttc aac cgc ttg cac acc aaa Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr Lys 150 155 160	540
atc tct att tta caa gat gag aaa ccc atc tat tat gac aac acg att Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile 165 170 175	588
tta gat ccc aaa acc acc gac tta aat aac atg tgc atg ttt gat ggc Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp Gly 180 185 190	636
tat acg cat tat ttg aat ttg gtg ctt gtc aat tgc ccc ata gag ctc Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu Leu 195 200 205	684
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gtg agt gaa acc gct agt tct cat tta tgc gtg aaa gct tta gcg aaa Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala Lys 230 235 240	780
ggc tca gaa ccc tta ttg cat tta aga gaa aaa atc gct cgc ttg gtt Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu Val 245 250 255	828
acg caa acc acc acg caa aag gtt tgaaagcact tcaaaaagat taaagtcctt Thr Gln Thr Thr Thr Gln Lys Val 260 265	882
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<212> PRT

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Leu	Arg	Glu	Gly	Met	Ser	Gln	Ser	Asn	Asn	Pro	Ser	Lys	Glu	Glu	Leu			
				55					60						65			
gat	cta	atc	atc	act	aac	gct	tta	atc	gtg	gat	tac	acc	ggg	att	tat		296	
Asp	Leu	Ile	Ile	Thr	Asn	Ala	Leu	Ile	Val	Asp	Tyr	Thr	Gly	Ile	Tyr			
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aaa	gcg	gat	att	ggg	att	aaa	gat	ggc	aaa	atc	gct	ggc	att	ggg	aaa		344	
Lys	Ala	Asp	Ile	Gly	Ile	Lys	Asp	Gly	Lys	Ile	Ala	Gly	Ile	Gly	Lys			
		85					90					95						
ggc	ggg	aac	aaa	gac	atg	caa	gat	ggc	gtt	aaa	aac	aat	ctt	agc	gta		392	
Gly	Gly	Asn	Lys	Asp	Met	Gln	Asp	Gly	Val	Lys	Asn	Asn	Leu	Ser	Val			
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ggg	cct	gct	act	gaa	gcc	tta	gcc	ggg	gaa	ggg	ttg	atc	gta	act	gct		440	
Gly	Pro	Ala	Thr	Glu	Ala	Leu	Ala	Gly	Glu	Gly	Leu	Ile	Val	Thr	Ala			
	115				120					125					130			
ggg	ggg	att	gac	aca	cac	atc	cac	ttc	att	tca	ccc	caa	caa	atc	cct		488	
Gly	Gly	Ile	Asp	Thr	His	Ile	His	Phe	Ile	Ser	Pro	Gln	Gln	Ile	Pro			
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aca	gct	ttt	gca	agc	ggg	gta	aca	acc	atg	att	ggg	ggc	gga	act	ggg		536	
Thr	Ala	Phe	Ala	Ser	Gly	Val	Thr	Thr	Met	Ile	Gly	Gly	Gly	Thr	Gly			
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cct	gct	gat	ggc	act	aat	gcg	act	act	atc	act	cca	ggc	aga	aga	aat		584	
Pro	Ala	Asp	Gly	Thr	Asn	Ala	Thr	Thr	Ile	Thr	Pro	Gly	Arg	Arg	Asn			
		165					170					175						
tta	aaa	tgg	atg	ctc	aga	gcg	gct	gaa	gaa	tat	tct	atg	aac	tta	ggg		632	
Leu	Lys	Trp	Met	Leu	Arg	Ala	Ala	Glu	Glu	Tyr	Ser	Met	Asn	Leu	Gly			
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ttc	ttg	gct	aaa	ggg	aac	gct	tct	aac	gac	gcg	agc	tta	gcc	gat	caa		680	
Phe	Leu	Ala	Lys	Gly	Asn	Ala	Ser	Asn	Asp	Ala	Ser	Leu	Ala	Asp	Gln			
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Ile	Glu	Ala	Gly	Ala	Ile	Gly	Phe	Lys	Ile	His	Glu	Asp	Trp	Gly	Thr			
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act	cct	tct	gca	atc	aat	cat	gcg	tta	gat	gtt	gca	gac	aaa	tac	gat		776	
Thr	Pro	Ser	Ala	Ile	Asn	His	Ala	Leu	Asp	Val	Ala	Asp	Lys	Tyr	Asp			
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gtg	caa	gtc	gct	atc	cac	aca	gac	act	ttg	aat	gaa	gcc	ggg	tgc	gtg		824	
Val	Gln	Val	Ala	Ile	His	Thr	Asp	Thr	Leu	Asn	Glu	Ala	Gly	Cys	Val			
		245					250					255						
gaa	gac	act	atg	gca	gct	att	gcc	gga	cgc	act	atg	cac	act	ttc	cac		872	
Glu	Asp	Thr	Met	Ala	Ala	Ile	Ala	Gly	Arg	Thr	Met	His	Thr	Phe	His			
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gcc ttt tta aaa caa atc aat ata gcc aga gtg gat tta agc acc ata Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser Thr Ile 195 200 205 210			680
gac aga ccc tca agc ttt aaa gcc cct aaa tta agc gaa gat gaa ttg Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp Glu Leu 215 220 225			728
tta aaa tgc tct tta ttt ttt gaa ggg ctt tgc gtg agt ttg cct aaa Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu Pro Lys 230 235 240			776
cga tcc att act caa gct aaa aaa ttg att tct tgc ggt ata gac gaa Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile Asp Glu 245 250 255			824
ttg ctc gct tta att tcc agg cgc cct tta agc gca gaa gaa gcc ccc Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu Ala Pro 260 265 270			872
cta att cta gat tct aac gct ttt aag cat tta gaa act ttg tta aac Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu Leu Asn 275 280 285 290			920
cat aag caa att acg att aaa aaa gtc ggc tct ttg gag ttt tat tgc His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe Tyr Cys 295 300 305			968
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aaa			1027
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Glu Arg Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile 50 55 60			
Gln Asn Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile 65 70 75 80			
Thr Ala Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile 85 90 95			
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[illegible]

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<221> CDS
<222> (87) ... (1280)
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                Met Glu Ser Val Lys Thr Gly Lys Thr
                1                5

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aat aag gtt ggc aag aat aca gag atg gct aat aca aag gca aat aaa 161  
Asn Lys Val Gly Lys Asn Thr Glu Met Ala Asn Thr Lys Ala Asn Lys  
10 15 20 25

gag act cat ttt aaa caa gtg agc gcc att aca aat ata atc aga tca 209  
Glu Thr His Phe Lys Gln Val Ser Ala Ile Thr Asn Ile Ile Arg Ser  
30 35 40

ggt ggt ggg ttt ttt aca aaa att gca aag aga gtt aga gga ctt gta 257  
Val Gly Gly Phe Phe Thr Lys Ile Ala Lys Arg Val Arg Gly Leu Val  
45 50 55

aaa aaa cac ccc aag aaa agc agt gcg gca tta gta gta ttg acc cat 305  
Lys Lys His Pro Lys Lys Ser Ser Ala Ala Leu Val Val Leu Thr His  
60 65 70

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tcc Ser 90	aaa Lys	caa Gln	gct Ala	gaa Glu	aaa Lys 95	gaa Glu	aat Asn	caa Gln	atc Ile	aat Asn 100	tgg Trp	tgg Trp	aaa Lys	tat Tyr	tca Ser 105	401
gga Gly	tta Leu	aca Thr	ata Ile	gcg Ala 110	gca Ala	agt Ser	tta Leu	tta Leu	tta Leu 115	gcc Ala	gct Ala	tgt Cys	agc Ser	gct Ala 120	ggc Gly	449
gat Asp	act Thr	gat Asp	aaa Lys 125	cag Gln	ata Ile	gaa Glu	cta Leu	gaa Glu	caa Gln	gaa Glu	aaa Lys	aag Lys	gaa Glu 135	gct Ala	gaa Glu	497
aac Asn	gct Ala	agg Arg 140	gat Asp	aga Arg	gcg Ala	aac Asn	aag Lys 145	agt Ser	ggg Gly	ata Ile	gaa Glu	cta Leu 150	gaa Glu	caa Gln	gaa Glu	545
aga Arg	cag Gln 155	aaa Lys	aca Thr	aac Asn	aag Lys	agt Ser 160	ggg Gly	ata Ile	gaa Glu	ctc Leu	gct Ala 165	aat Asn	agt Ser	caa Gln	ata Ile	593
aaa Lys 170	gca Ala	gaa Glu	caa Gln	gaa Glu	aga Arg 175	caa Gln	aag Lys	aca Thr	gaa Glu	caa Gln 180	gaa Glu	aaa Lys	caa Gln	aaa Lys	gca Ala 185	641
aat Asn	aag Lys	agt Ser	gcg Ala	ata Ile 190	gag Glu	tta Leu	gaa Glu	cag Gln	caa Gln 195	aaa Lys	caa Gln	aag Lys	acc Thr 200	att Ile	aat Asn	689
aca Thr	caa Gln	aga Arg	gat Asp 205	ttg Leu	att Ile	aaa Lys	gaa Glu	cag Gln 210	aaa Lys	gat Asp	ttc Phe	att Ile	aaa Lys 215	gaa Glu	aca Thr	737
gaa Glu	caa Gln	aat Asn 220	tgc Cys	caa Gln	gaa Glu	aat Asn	cat His 225	aat Asn	caa Gln	ttc Phe	ttt Phe 230	att Ile	aaa Lys	aaa Lys	tta Leu	785
gga Gly	att Ile 235	aag Lys	ggc Gly	ggc Gly	att Ile	gct Ala 240	ata Ile	gaa Glu	gta Val	gaa Glu	gct Ala 245	gaa Glu	tgc Cys	aaa Lys	acc Thr	833
cct Pro 250	aaa Lys	cct Pro	gca Ala	aaa Lys	acc Thr 255	aat Asn	caa Gln	acc Thr	cct Pro	atc Ile 260	cag Gln	cca Pro	aaa Lys	cac His	ctc Leu 265	881
cca Pro	aac Asn	tct Ser	aaa Lys	caa Gln 270	cct Pro	cat His	tct Ser	caa Gln	aga Arg 275	gga Gly	tca Ser	aaa Lys	gcg Ala 280	caa Gln	gag Glu	929
ttt Phe	atc Ile	gct Ala	tat Tyr 285	ttg Leu	caa Gln	aaa Lys	gag Glu	cta Leu	gaa Glu 290	ttt Phe	ctg Leu	ccc Pro	tat Tyr 295	tcg Ser	caa Gln	977
aaa Lys	gct Ala	atc Ile 300	gct Ala	aaa Lys	caa Gln	gtg Val	aat Asn 305	ttc Phe	tat Tyr	aaa Lys	cca Pro	agt Ser 310	tct Ser	atc Ile	gct Ala	1025





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Tyr	Asp	Phe 85	Lys	Thr	Ser	Ser	Lys 90	Ile	Ser	Glu	Glu	Asp 95	Leu	Pro	Lys	
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Ile	Glu 100	Ala	Lys	Met	Lys	Glu 105	Phe	Ala	Lys	Leu	Lys 110	Leu	Ala	Ile	Thr	
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Lys 115	Glu	Thr	Leu	Thr	Arg 120	Glu	Gln	Ala	Leu	Glu 125	Arg	Phe	Lys	Gly 130	Asp	
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Glu	Leu	Lys	His 135	Ala	Val	Met	Ser	Lys	Ile 140	Gly	Gly	Asp	Ala	Phe 145	Gly	
gtg	tat	caa	caa	ggc	gag	ttt	gaa	gat	ttg	tgt	aag	ggg	cgc	cat	ctc	536
Val	Tyr	Gln 150	Gln	Gly	Glu	Phe	Glu 155	Asp	Leu	Cys	Lys	Gly 160	Pro	His	Leu	
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Pro	Asn 165	Thr	Arg	Phe	Leu	Asn 170	His	Phe	Lys	Leu	Thr 175	Lys	Leu	Ala	Gly	
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Ala	Tyr 180	Leu	Gly	Gly	Asp 185	Glu	Asn	Asn	Glu	Met 190	Leu	Ile	Arg	Ile	Tyr	
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Gly 195	Ile	Ala	Phe	Ala 200	Thr	Lys	Glu	Gly	Leu 205	Lys	Asp	Tyr	Leu	Phe 210	Gln	
ata	gaa	gaa	gcg	aaa	aaa	cga	gat	cac	aga	aag	cta	ggc	gtg	gag	cta	728
Ile	Glu	Glu	Ala 215	Lys	Lys	Arg	Asp	His 220	Arg	Lys	Leu	Gly	Val 225	Glu	Leu	
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Gly	Leu	Phe 230	Ser	Phe	Asp	Asp	Glu 235	Ile	Gly	Ala	Gly	Leu 240	Pro	Leu	Trp	
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Leu	Pro 245	Lys	Gly	Ala	Arg	Leu 250	Arg	Lys	Arg	Ile	Glu 255	Asp	Leu	Leu	Ser	
caa	gcg	tta	ctt	tta	aga	ggc	tat	gag	cgc	gtt	aaa	ggg	cct	gag	att	872
Gln 260	Ala	Leu	Leu	Leu	Arg 265	Gly	Tyr	Glu	Pro 270	Val	Lys 275	Gly	Pro	Glu	Ile	
tta	aag	agc	gat	gtg	tgg	aaa	atc	agc	ggg	cat	tat	gac	aac	tat	aaa	920
Leu 275	Lys	Ser	Asp	Val 280	Trp	Lys	Ile	Ser	Gly 285	His	Tyr	Asp	Asn	Tyr 290	Lys	
gaa	aac	atg	tat	ttc	acc	acg	att	gat	gag	caa	gaa	tat	ggc	ata	aag	968
Glu	Asn 295	Met	Tyr	Phe	Thr	Thr	Ile	Asp 300	Glu	Gln	Glu	Tyr 305	Gly	Ile	Lys	
cct	atg	aac	tgc	gtg	ggg	cat	att	aaa	gtc	tat	caa	agc	gct	ttg	cac	1016
Pro	Met	Asn 310	Cys	Val	Gly	His 315	Ile	Lys 320	Val	Tyr	Gln	Ser 325	Ala	Leu	His	

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Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val Val His	
325 330 335	
cgg cat gaa aaa agc ggc gtg ttg cat ggg ctt tta agg gtt agg gaa	1112
Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val Arg Glu	
340 345 350	
ttt acc caa gat gat gca cat att ttt tgc tct ttt gaa cag atc caa	1160
Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln Ile Gln	
355 360 365 370	
agc gaa gtg agc gcg att tta gat ttt acg cac aaa atc atg caa gcg	1208
Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met Gln Ala	
375 380 385	
ttt gat ttt agc tat gaa atg gaa tta tcc aca agg ccg gct aaa tcc	1256
Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala Lys Ser	
390 395 400	
ata ggc gat gat aaa gtt tgg gaa aag gcc act aac gct tta aaa gaa	1304
Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu Lys Glu	
405 410 415	
gcc tta aaa gaa cac cgc att gat tac aag att gat gaa ggg gga ggg	1352
Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly Gly Gly	
420 425 430	
gct ttc tat ggg cct aag att gac att aaa atc act gac gct tta aag	1400
Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala Leu Lys	
435 440 445 450	
cgt aaa tgg cag tgt ggc acg att caa gtg gat atg aat ttg cct gaa	1448
Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu Pro Glu	
455 460 465	
cgc ttc aag ctc gct ttc act aat gag tat aat cac gct gag cag ccg	1496
Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu Gln Pro	
470 475 480	
gtg atg atc cac aga gcg att tta ggc tcg ttt gaa agg ttt att gcg	1544
Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe Ile Ala	
485 490 495	
att ttg agc gaa cat ttt ggg ggg aat ttc cct ttc ttt gtc gcg ccc	1592
Ile Leu Ser Glu His Phe Gly Gly Asn Phe Pro Phe Phe Val Ala Pro	
500 505 510	
act caa atc gct ctc atc cct att aat gaa gag cat cat gtt ttt gct	1640
Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val Phe Ala	
515 520 525 530	
ttg aaa tta aaa gag gcg cta aaa aag cgc gat att ttt gta gaa gtg	1688
Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val Glu Val	
535 540 545	
tta gat aaa aac gac agc ttg aat aaa aag gtg cga tta gcc gaa aag	1736
Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala Glu Lys	



550	555	560	
caa aaa atc cct atg att tta gtg tta ggg aat gaa gaa gtg gag acc			1784
Gln Lys Ile Pro Met Ile Leu Val Leu Gly Asn Glu Glu Val Glu Thr			
565	570	575	
gaa att tta tcc att aga gac aga gaa aaa caa gat caa tat aaa atg			1832
Glu Ile Leu Ser Ile Arg Asp Arg Glu Lys Gln Asp Gln Tyr Lys Met			
580	585	590	
ccc tta aag gag ttt tta aac atg gtt gaa tct aag atg caa gag gtt			1880
Pro Leu Lys Glu Phe Leu Asn Met Val Glu Ser Lys Met Gln Glu Val			
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cgt			1939
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Asn Gly Thr Glu Pro Ile Tyr Phe Asp Asp Ser Pro Leu Ala Leu Glu			
35 40 45			
Val Ile Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala			
50 55 60			
Leu Tyr Pro Asp Ala Lys Phe Phe Val Gly Pro Val Val Glu Glu Gly			
65 70 75 80			
Phe Tyr Tyr Asp Phe Lys Thr Ser Ser Lys Ile Ser Glu Glu Asp Leu			
85 90 95			
Pro Lys Ile Glu Ala Lys Met Lys Glu Phe Ala Lys Leu Lys Leu Ala			
100 105 110			
Ile Thr Lys Glu Thr Leu Thr Arg Glu Gln Ala Leu Glu Arg Phe Lys			
115 120 125			
Gly Asp Glu Leu Lys His Ala Val Met Ser Lys Ile Gly Gly Asp Ala			
130 135 140			
Phe Gly Val Tyr Gln Gln Gly Glu Phe Glu Asp Leu Cys Lys Gly Pro			
145 150 155 160			
His Leu Pro Asn Thr Arg Phe Leu Asn His Phe Lys Leu Thr Lys Leu			
165 170 175			
Ala Gly Ala Tyr Leu Gly Gly Asp Glu Asn Asn Glu Met Leu Ile Arg			
180 185 190			
Ile Tyr Gly Ile Ala Phe Ala Thr Lys Glu Gly Leu Lys Asp Tyr Leu			
195 200 205			
Phe Gln Ile Glu Glu Ala Lys Lys Arg Asp His Arg Lys Leu Gly Val			
210 215 220			
Glu Leu Gly Leu Phe Ser Phe Asp Asp Glu Ile Gly Ala Gly Leu Pro			
225 230 235 240			
Leu Trp Leu Pro Lys Gly Ala Arg Leu Arg Lys Arg Ile Glu Asp Leu			
245 250 255			
Leu Ser Gln Ala Leu Leu Leu Arg Gly Tyr Glu Pro Val Lys Gly Pro			

Glu	Ile	Leu	Lys	Ser	Asp	Val	Trp	Lys	Ile	Ser	Gly	His	Tyr	Asp	Asn	
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Tyr	Lys	Glu	Asn	Met	Tyr	Phe	Thr	Thr	Ile	Asp	Glu	Gln	Glu	Tyr	Gly	
	290					295					300					
Ile	Lys	Pro	Met	Asn	Cys	Val	Gly	His	Ile	Lys	Val	Tyr	Gln	Ser	Ala	
305					310					315					320	
Leu	His	Ser	Tyr	Arg	Asp	Leu	Pro	Leu	Arg	Phe	Tyr	Glu	Tyr	Gly	Val	
				325					330					335		
Val	His	Arg	His	Glu	Lys	Ser	Gly	Val	Leu	His	Gly	Leu	Leu	Arg	Val	
			340					345					350			
Arg	Glu	Phe	Thr	Gln	Asp	Asp	Ala	His	Ile	Phe	Cys	Ser	Phe	Glu	Gln	
		355					360					365				
Ile	Gln	Ser	Glu	Val	Ser	Ala	Ile	Leu	Asp	Phe	Thr	His	Lys	Ile	Met	
	370					375					380					
Gln	Ala	Phe	Asp	Phe	Ser	Tyr	Glu	Met	Glu	Leu	Ser	Thr	Arg	Pro	Ala	
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Lys	Ser	Ile	Gly	Asp	Asp	Lys	Val	Trp	Glu	Lys	Ala	Thr	Asn	Ala	Leu	
				405				410						415		
Lys	Glu	Ala	Leu	Lys	Glu	His	Arg	Ile	Asp	Tyr	Lys	Ile	Asp	Glu	Gly	
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Gly	Gly	Ala	Phe	Tyr	Gly	Pro	Lys	Ile	Asp	Ile	Lys	Ile	Thr	Asp	Ala	
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Leu	Lys	Arg	Lys	Trp	Gln	Cys	Gly	Thr	Ile	Gln	Val	Asp	Met	Asn	Leu	
	450					455					460					
Pro	Glu	Arg	Phe	Lys	Leu	Ala	Phe	Thr	Asn	Glu	Tyr	Asn	His	Ala	Glu	
465					470					475					480	
Gln	Pro	Val	Met	Ile	His	Arg	Ala	Ile	Leu	Gly	Ser	Phe	Glu	Arg	Phe	
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Ile	Ala	Ile	Leu	Ser	Glu	His	Phe	Gly	Gly	Asn	Phe	Pro	Phe	Phe	Val	
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Ala	Pro	Thr	Gln	Ile	Ala	Leu	Ile	Pro	Ile	Asn	Glu	Glu	His	His	Val	
		515					520					525				
Phe	Ala	Leu	Lys	Leu	Lys	Glu	Ala	Leu	Lys	Lys	Arg	Asp	Ile	Phe	Val	
	530					535					540					
Glu	Val	Leu	Asp	Lys	Asn	Asp	Ser	Leu	Asn	Lys	Lys	Val	Arg	Leu	Ala	
545					550					555					560	
Glu	Lys	Gln	Lys	Ile	Pro	Met	Ile	Leu	Val	Leu	Gly	Asn	Glu	Glu	Val	
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Glu	Thr	Glu	Ile	Leu	Ser	Ile	Arg	Asp	Arg	Glu	Lys	Gln	Asp	Gln	Tyr	
			580					585					590			
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<212> DNA
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Lys Val Met Met Gln Met Ala Ile Val Leu Thr Phe Ala Gly Ser Ile	
5 10 15	
ccg atc gtg aaa gtg ggg cgc att gcc ggg caa ttt gcc aag cct cgc	152
Pro Ile Val Lys Val Gly Arg Ile Ala Gly Gln Phe Ala Lys Pro Arg	
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Ser Asn Ala Thr Glu Met Leu Asp Asn Glu Glu Val Leu Ser Tyr Arg	
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Gly Asp Ile Ile Asn Gly Ile Ser Lys Lys Glu Arg Glu Pro Asn Pro	
55 60 65	
gaa aga atg ctt aag gcc tac cat caa agc gta gcg act tta aac ctt	296
Glu Arg Met Leu Lys Ala Tyr His Gln Ser Val Ala Thr Leu Asn Leu	
70 75 80	
atc aga gcc ttt gct caa ggc ggg tta gcg gat ttg gag caa gtg cat	344
Ile Arg Ala Phe Ala Gln Gly Gly Leu Ala Asp Leu Glu Gln Val His	
85 90 95	
cgt ttc aat ttg gat ttt gtc aaa aac aac gac ttt ggg caa aaa tac	392
Arg Phe Asn Leu Asp Phe Val Lys Asn Asn Asp Phe Gly Gln Lys Tyr	
100 105 110	
cag caa atc gct gac cgg atc acg caa gct tta ggg ttt atg cga gca	440
Gln Gln Ile Ala Asp Arg Ile Thr Gln Ala Leu Gly Phe Met Arg Ala	
115 120 125 130	
tgc ggg gtg gag ata gag cga acg cct att ctt agg gaa gtg gaa ttt	488
Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val Glu Phe	
135 140 145	
tac acc agc cac gaa gcg tta ctg ctc cat tat gaa gag ccg ttg gtg	536
Tyr Thr Ser His Glu Ala Leu Leu Leu His Tyr Glu Glu Pro Leu Val	
150 155 160	
cgt aag gat agt ctg act aac cag ttt tat gat tgc tcc gcg cac atg	584
Arg Lys Asp Ser Leu Thr Asn Gln Phe Tyr Asp Cys Ser Ala His Met	
165 170 175	
cta tgg att ggc gaa agg aca aga gac cct aag ggt gcg cat gtg gag	632
Leu Trp Ile Gly Glu Arg Thr Arg Asp Pro Lys Gly Ala His Val Glu	
180 185 190	
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Phe Leu Arg Gly Val Cys Asn Pro Ile Gly Val Lys Ile Gly Pro Asn	
195 200 205 210	
gcg agc gtg agc gaa gtg tta gaa ttg tgc gat gtt tta aac ccg cgc	728
Ala Ser Val Ser Glu Val Leu Glu Leu Cys Asp Val Leu Asn Pro Arg	
215 220 225	
aac att aag ggg cgt ttg aat ttg atc gtg cgc atg ggt tct aag atg	776
Asn Ile Lys Gly Arg Leu Asn Leu Ile Val Arg Met Gly Ser Lys Met	

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		245					250					255							
cgc Arg	cat His	att Ile	tta Leu	tgg Trp	agc Ser	att Ile	gat Asp	ccc Pro	atg Met	cat His	ggc Gly	aac Asn	acg Thr	gtt Val	aaa Lys			872	
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acc Thr	agc Ser	ttg Leu	ggg Gly	gtt Val	aaa Lys	aca Thr	agg Arg	gct Ala	ttt Phe	gat Asp	agc Ser	gtg Val	tta Leu	gat Asp	gaa Glu			920	
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gtg Val	aaa Lys	agc Ser	ttt Phe	ttt Phe	gaa Glu	atc Ile	cat His	agg Arg	gct Ala	gaa Glu	ggg Gly	agt Ser	ttg Leu	gct Ala	tca Ser			968	
				295					300					305					
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			325					330				335							
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Pro	Arg	Ser	Asn	Ala	Thr	Glu	Met	Leu	Asp	Asn	Glu	Glu	Val	Leu	Ser				
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Tyr	Arg	Gly	Asp	Ile	Ile	Asn	Gly	Ile	Ser	Lys	Lys	Glu	Arg	Glu	Pro				
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ccc aag ctt gaa atc cca caa acc cca tgc aat aaa gcc gta tca atc 296  
Pro Lys Leu Glu Ile Pro Gln Thr Pro Cys Asn Lys Ala Val Ser Ile  
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tca aac aac tct tca cgc atc gct tca att tct tta tca taaggctgta 345  
Ser Asn Asn Ser Ser Arg Ile Ala Ser Ile Ser Leu Ser  
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35 40 45  
Val Met Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro  
50 55 60  
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Glu Phe His Gln Ile Tyr Asp Pro Leu Gly Asn Ile Trp Leu Ser Ala  
5 10 15

ctt gtg gcc tta ttg ccg att tta ttg ttt ttc tta tct tta atg gtt 152  
Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu Met Val  
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Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala Leu Ser  
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gcc gtt att gcg gtt tta gtg tat aaa atg cct gtt agc atg gtg ggt 248  
Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met Val Gly  
55 60 65

tca agc ttc ctt tac ggc ttt ctt tat ggc tta tgg ccg atc gct tgg	296
Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala Trp	
70 75 80	
atc att att gcg gcg att ttt tta tac aaa ctc agc gtt aaa tcc ggc	344
Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys Ser Gly	
85 90 95	
tat ttt gaa att tta aaa gaa agc gtc cag tcc atc act tta gat cac	392
Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu Asp His	
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cgc att tta gtg att ttg att ggc ttt tgt ttt ggc tgc ttt tta gaa	440
Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu Glu	
115 120 125 130	
ggg gcg atc ggc ttt gga ggg cct att gcc att acc gca gcg att tta	488
Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala Ile Leu	
135 140 145	
gtg ggc tta ggg tta agc cct ttg tat tct gcc ggg tta tgt ttg atc	536
Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys Leu Ile	
150 155 160	
gct aat acc gct cct gta gct ttt ggc gcg gtg ggt atc cct ata agt	584
Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro Ile Ser	
165 170 175	
gct atg gcg agc gcg gta ggg gtg cca gcg att tta att tca gcc atg	632
Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser Ala Met	
180 185 190	
acg ggt aaa atc ctc ttt ttt gtg agc ttg tta gtg ccg ttt ttc att	680
Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe Phe Ile	
195 200 205 210	
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Val Phe Leu Met Asp Gly Phe Lys Gly Ile Lys Glu Thr Phe Pro Ala	
215 220 225	
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Val Phe Ile Ala Ala Phe Ser Phe Ala Gly Ala Gln Phe Leu Ser Ser	
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Asn Tyr Leu Gly Pro Glu Leu Pro Gly Ile Ile Ser Ala Leu Val Ser	
245 250 255	
ctc gtt gca aca gcg ctc ttt ttg aaa ttt tgg cag cct aaa gcg att	872
Leu Val Ala Thr Ala Leu Phe Leu Lys Phe Trp Gln Pro Lys Ala Ile	
260 265 270	
ttt aga agc gac ggc aaa gcg gct tgc ttc act aag agt aac cat cat	920
Phe Arg Ser Asp Gly Lys Ala Ala Ser Phe Thr Lys Ser Asn His His	
275 280 285 290	
att tgt aag atc tat gtc gct tgg tct cct ttt gtg att tta gtt tta	968
Ile Cys Lys Ile Tyr Val Ala Trp Ser Pro Phe Val Ile Leu Val Leu	

				295				300				305							
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Val	Ile	Val	Leu	Trp	Ile	Gln	Pro	Phe	Phe	Lys	Ala	Leu	Phe	Glu	Lys				
				310				315				320							
gac	ggc	ttg	tta	gct	ttt	tct	aat	ttt	tat	ttt	gaa	ttc	aat	aac	atc		1064		
Asp	Gly	Leu	Leu	Ala	Phe	Ser	Asn	Phe	Tyr	Phe	Glu	Phe	Asn	Asn	Ile				
				325				330				335							
agt	aac	cac	atc	ttt	aaa	agc	ccg	cct	ttt	gta	gaa	gcc	aat	caa	agc		1112		
Ser	Asn	His	Ile	Phe	Lys	Ser	Pro	Pro	Phe	Val	Glu	Ala	Asn	Gln	Ser				
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Val	Ser	Phe	Pro	Val	Val	Phe	Lys	Phe	Leu	Leu	Ile	Asn	Thr	Val	Gly				
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Thr	Ser	Ile	Phe	Leu	Ala	Ala	Leu	Val	Ser	Met	Leu	Val	Leu	Arg	Val				
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cga	gtg	agc	gat	gcg	ctg	agc	gtc	ttt	ggc	gag	act	tta	aaa	gaa	atg		1256		
Arg	Val	Ser	Asp	Ala	Leu	Ser	Val	Phe	Gly	Glu	Thr	Leu	Lys	Glu	Met				
				390				395				400							
cgt	tac	ccc	att	ctc	acc	att	ggg	tta	gtc	tta	agc	ttt	gcc	tat	gtg		1304		
Arg	Tyr	Pro	Ile	Leu	Thr	Ile	Gly	Leu	Val	Leu	Ser	Phe	Ala	Tyr	Val				
				405				410				415							
tct	aat	tac	agc	ggg	att	tct	tcc	act	cta	gcc	tta	gcg	ctc	acg	cat		1352		
Ser	Asn	Tyr	Ser	Gly	Ile	Ser	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Thr	His				
				420				425				430							
acg	ggg	ttg	gct	ttc	acc	ttt	ttc	tcg	ccc	ttg	atc	ggg	tgg	gta	ggc		1400		
Thr	Gly	Leu	Ala	Phe	Thr	Phe	Phe	Ser	Pro	Leu	Ile	Gly	Trp	Val	Gly				
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gtg	ttt	tta	acc	ggg	agc	gat	acg	agt	tcc	aat	ctt	ttg	ttt	ggc	tct		1448		
Val	Phe	Leu	Thr	Gly	Ser	Asp	Thr	Ser	Ser	Asn	Leu	Leu	Phe	Gly	Ser				
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tta	cag	caa	ctc	acc	gcc	caa	cga	ttg	cac	ctc	cct	gag	gtt	tta	acc		1496		
Leu	Gln	Gln	Leu	Thr	Ala	Gln	Arg	Leu	His	Leu	Pro	Glu	Val	Leu	Thr				
				470				475				480							
cta	acg	gct	aat	acc	gtg	ggg	ggc	act	tta	ggc	aag	atg	ata	agc	cct		1544		
Leu	Thr	Ala	Asn	Thr	Val	Gly	Gly	Thr	Leu	Gly	Lys	Met	Ile	Ser	Pro				
				485				490				495							
caa	agc	atc	gct	atc	gct	tgc	gcg	gcg	gtg	ggg	tta	gcc	ggg	aaa	gag		1592		
Gln	Ser	Ile	Ala	Ile	Ala	Cys	Ala	Ala	Val	Gly	Leu	Ala	Gly	Lys	Glu				
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agc	gat	ttg	ttc	aaa	ttc	acg	gtt	aaa	tac	tcc	ctt	att	ttt	gta	gcg		1640		
Ser	Asp	Leu	Phe	Lys	Phe	Thr	Val	Lys	Tyr	Ser	Leu	Ile	Phe	Val	Ala				
				515				520				525				530			
atc	atg	gga	gtt	gtg															



Ile Met Gly Val Val Ile Ser Ala Ile Ala Tyr Leu Ile Pro Glu Val  
535 540 545

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<213> Helicobacter pylori

<400> 268

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Met	Val	Phe	Lys	Leu	Lys	Gly	Tyr	Thr	Ala	Ala	Phe	Leu	Ser	Val	Ala
	35						40					45			
Leu	Ser	Ala	Val	Ile	Ala	Val	Leu	Val	Tyr	Lys	Met	Pro	Val	Ser	Met
	50					55					60				
Val	Gly	Ser	Ser	Phe	Leu	Tyr	Gly	Phe	Leu	Tyr	Gly	Leu	Trp	Pro	Ile
65					70					75				80	
Ala	Trp	Ile	Ile	Ile	Ala	Ala	Ile	Phe	Leu	Tyr	Lys	Leu	Ser	Val	Lys
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Ser	Gly	Tyr	Phe	Glu	Ile	Leu	Lys	Glu	Ser	Val	Gln	Ser	Ile	Thr	Leu
			100					105					110		
Asp	His	Arg	Ile	Leu	Val	Ile	Leu	Ile	Gly	Phe	Cys	Phe	Gly	Ser	Phe
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Leu	Glu	Gly	Ala	Ile	Gly	Phe	Gly	Gly	Pro	Ile	Ala	Ile	Thr	Ala	Ala
	130					135					140				
Ile	Leu	Val	Gly	Leu	Gly	Leu	Ser	Pro	Leu	Tyr	Ser	Ala	Gly	Leu	Cys
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Leu	Ile	Ala	Asn	Thr	Ala	Pro	Val	Ala	Phe	Gly	Ala	Val	Gly	Ile	Pro
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Ile	Ser	Ala	Met	Ala	Ser	Ala	Val	Gly	Val	Pro	Ala	Ile	Leu	Ile	Ser
			180					185					190		
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	195						200					205			
Phe	Ile	Val	Phe	Leu	Met	Asp	Gly	Phe	Lys	Gly	Ile	Lys	Glu	Thr	Phe
	210					215					220				
Pro	Ala	Val	Phe	Ile	Ala	Ala	Phe	Ser	Phe	Ala	Gly	Ala	Gln	Phe	Leu
225					230					235				240	
Ser	Ser	Asn	Tyr	Leu	Gly	Pro	Glu	Leu	Pro	Gly	Ile	Ile	Ser	Ala	Leu
				245					250					255	
Val	Ser	Leu	Val	Ala	Thr	Ala	Leu	Phe	Leu	Lys	Phe	Trp	Gln	Pro	Lys
			260					265					270		
Ala	Ile	Phe	Arg	Ser	Asp	Gly	Lys	Ala	Ala	Ser	Phe	Thr	Lys	Ser	Asn
		275					280					285			
His	His	Ile	Cys	Lys	Ile	Tyr	Val	Ala	Trp	Ser	Pro	Phe	Val	Ile	Leu
	290					295					300				
Val	Leu	Val	Ile	Val	Leu	Trp	Ile	Gln	Pro	Phe	Phe	Lys	Ala	Leu	Phe
	305				310					315				320	
Glu	Lys	Asp	Gly	Leu	Leu	Ala	Phe	Ser	Asn	Phe	Tyr	Phe	Glu	Phe	Asn
				325					330					335	
Asn	Ile	Ser	Asn	His	Ile	Phe	Lys	Ser	Pro	Pro	Phe	Val	Glu	Ala	Asn
			340					345					350		

Gln Ser Val Ser Phe Pro Val Val Phe Lys Phe Leu Leu Ile Asn Thr  
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 385 390 395 400  
 Glu Met Arg Tyr Pro Ile Leu Thr Ile Gly Leu Val Leu Ser Phe Ala  
 405 410 415  
 Tyr Val Ser Asn Tyr Ser Gly Ile Ser Ser Thr Leu Ala Leu Ala Leu  
 420 425 430  
 Thr His Thr Gly Leu Ala Phe Thr Phe Phe Ser Pro Leu Ile Gly Trp  
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 Val Gly Val Phe Leu Thr Gly Ser Asp Thr Ser Ser Asn Leu Leu Phe  
 450 455 460  
 Gly Ser Leu Gln Gln Leu Thr Ala Gln Arg Leu His Leu Pro Glu Val  
 465 470 475 480  
 Leu Thr Leu Thr Ala Asn Thr Val Gly Gly Thr Leu Gly Lys Met Ile  
 485 490 495  
 Ser Pro Gln Ser Ile Ala Ile Ala Cys Ala Ala Val Gly Leu Ala Gly  
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 Lys Glu Ser Asp Leu Phe Lys Phe Thr Val Lys Tyr Ser Leu Ile Phe  
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 Arg Asp Ser Lys Ser Gln Gly Glu Leu Val Glu Asn Gly His Leu Ile  
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 Asp Gly Ile Gly Glu Phe Ala Asn Asn Val Pro Val Gly Trp Ile Ala  
 55 60 65  
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Tyr	Pro	Leu	Asn	Ser	Phe	Ser	Gln	Ile	Gly	Gln	Tyr	Asn	Glu	Glu	Val	
		85					90					95				
aaa	gcg	cac	aac	caa	aaa	ttt	gag	gcc	aag	tgg	aag	cat	ttg	ggg	caa	392
Lys	Ala	His	Asn	Gln	Lys	Phe	Glu	Ala	Lys	Trp	Lys	His	Leu	Gly	Gln	
	100					105					110					
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Lys	Glu	Leu	Val	Asp	Met	Gly	Gln	Gly	Ile	Phe	Leu	Val	His	Cys	Ser	
	115				120					125					130	
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Gln	Cys	His	Gly	Ile	Thr	Ala	Glu	Gly	Leu	His	Gly	Ser	Ala	Gln	Asn	
				135					140					145		
ctg	gtg	cg	tgg	ggg	aaa	gaa	gag	ggg	att	atg	gat	acc	att	aag	cat	536
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			150					155					160			
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Gly	Ser	Lys	Gly	Met	Asp	Tyr	Leu	Ala	Gly	Glu	Met	Pro	Ala	Met	Glu	
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Leu	Asp	Glu	Lys	Asp	Ala	Lys	Ala	Ile	Ala	Ser	Tyr	Val	Met	Ala	Glu	
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Leu	Ser	Ser	Val	Lys	Lys	Thr	Lys	Asn	Pro	Gln	Leu	Ile	Asp	Lys	Gly	
	195				200					205					210	
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Lys	Glu	Leu	Phe	Glu	Ser	Met	Gly	Cys	Thr	Gly	Cys	His	Gly	Asn	Asp	
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ggg	aag	ggc	ttg	caa	gaa	aat	caa	gtg	ttt	gca	ggc	gat	ttg	acc	gct	776
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Tyr	Gly	Thr	Glu	Asn	Phe	Leu	Arg	Asn	Ile	Leu	Thr	His	Gly	Lys	Lys	
		245					250					255				
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Gly	Asn	Ile	Gly	His	Met	Pro	Ser	Phe	Lys	Tyr	Lys	Asn	Phe	Ser	Asp	
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<213> Helicobacter pylori

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130 135 140  
Gln Asn Leu Val Arg Trp Gly Lys Glu Glu Gly Ile Met Asp Thr Ile  
145 150 155 160  
Lys His Gly Ser Lys Gly Met Asp Tyr Leu Ala Gly Glu Met Pro Ala  
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180 185 190  
Ala Glu Leu Ser Ser Val Lys Lys Thr Lys Asn Pro Gln Leu Ile Asp  
195 200 205  
Lys Gly Lys Glu Leu Phe Glu Ser Met Gly Cys Thr Gly Cys His Gly  
210 215 220  
Asn Asp Gly Lys Gly Leu Gln Glu Asn Gln Val Phe Ala Ala Asp Leu  
225 230 235 240  
Thr Ala Tyr Gly Thr Glu Asn Phe Leu Arg Asn Ile Leu Thr His Gly  
245 250 255  
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<211> 307

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1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775

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gcg att aaa aga gcg agc agt aaa gaa ggg aat ttg agt gaa atc act Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu Ile Thr 70 75 80	296
tat gaa ggt aag gcg aat ttt ggc gtg cta atc atc atg gaa tgc atg Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu Cys Met 85 90 95	344
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<213> Helicobacter pylori

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Ala	Ala	Lys	Asp	Gly	Gly	Ser	Glu	Pro	Asp	Thr	Asn	Ala	Lys	Leu	Arg
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Ile	Thr	Tyr	Glu	Gly	Lys	Ala	Asn	Phe	Gly	Val	Leu	Ile	Ile	Met	Glu
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Cys	Met	Thr	Asp	Asn	Pro	Thr	Arg	Thr	Ile	Ala	Asn	Leu	Lys	Ser	Tyr
			100					105					110		
Phe	Asn	Lys	Thr	Gln	Gly	Ala	Ser	Ile	Val	Pro	Asn	Gly	Ser	Leu	Glu
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Tyr	Gly	Leu	Glu	Glu	Leu	Glu	Glu	Val	Glu	Asp	Lys	Ile	Ile	Ile	Arg
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			180					185					190		
Lys	Leu	Pro	Ile	Leu	Lys	Ala	Ser	Leu	Gln	Arg	Ile	Ala	Thr	Thr	Pro
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gct aag aat			gaa gac		aac aaa		aaa ttg		tat gac		atc att		gac ggc		cag		164
Ala Lys Asn			Glu Asp		Asn Lys		Lys Leu		Tyr Asp		Ile Ile		Asp Gly		Gln		
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Gln Arg Thr			Thr Thr		Ile Phe		Met Leu		Leu Leu		His Val		Leu Ala		Asn Lys		
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Gln Asn Glu			Lys Asp		Lys Gln		Glu Thr		Arg Lys		Tyr Leu		Tyr Tyr		Gln Lys		
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ggg gaa tta			aaa tta		gaa gtc		gcc ccc		aaa aac		caa agc		ttc ttc		aaa		308
Gly Glu Leu			Lys Leu		Glu Val		Ala Pro		Lys Asn		Gln Ser		Phe Phe		Lys		

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Thr Leu Leu Glu Ala Ala Glu Lys Glu Asn Ile Ser Gln Lys Lys Met						
	70		75		80	
cag aca ccg agg gca agc aaa atc ttt ttg aag ttt tgaaggctat						402
Gln Thr Pro Arg Ala Ser Lys Ile Phe Leu Lys Phe						
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Tyr Gln Lys Gly Glu Leu Lys Leu Glu Val Ala Pro Lys Asn Gln Ser						
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Gln Ser Ala Val Ser Lys Pro His Phe Lys Glu Tyr Gln Leu Lys Glu						
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Thr Pro Ser Met Thr Leu Phe Ile Ala Leu Asn Leu Ile Arg Glu His						
35 40 45						
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Gln Asp Pro Asp Leu Ser Phe Asp Phe Val Cys Arg Ala Gly Ile Cys						



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Gly Ser Cys Ala Met Met Val Asn Gly Arg Pro Arg Leu Ala Cys Lys	70	75	80	
acc cta act tct agc ttt gaa agc ggg gtg atc acg ctc atg ccc atg				344
Thr Leu Thr Ser Ser Phe Glu Ser Gly Val Ile Thr Leu Met Pro Met	85	90	95	
ccc agt ttt acg ctc att aaa gat ttg agc gtg aat acg ggc gat tgg				392
Pro Ser Phe Thr Leu Ile Lys Asp Leu Ser Val Asn Thr Gly Asp Trp	100	105	110	
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Phe Leu Asp Met Thr Lys Arg Val Glu Ser Trp Ala His Ser Lys Glu	115	120	125	
gaa gtg gat att act aga ccg gaa aaa agg gtt gag cct gac gaa gcc				488
Glu Val Asp Ile Thr Arg Pro Glu Lys Arg Val Glu Pro Asp Glu Ala	130	135	140	145
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Gln Glu Val Phe Glu Leu Asp Arg Cys Ile Glu Cys Gly Cys Cys Ile	150	155	160	
gct tct tgc ggg act aaa ctc atg cgc cct aat ttc att gga gct gct				584
Ala Ser Cys Gly Thr Lys Leu Met Arg Pro Asn Phe Ile Gly Ala Ala	165	170	175	
ggc atg aac aga gcc atg cgt ttt atg att gac agc cac gat gaa aga				632
Gly Met Asn Arg Ala Met Arg Phe Met Ile Asp Ser His Asp Glu Arg	180	185	190	
aac gat gat gat ttt tat gag tta gtc ggc gat gat gat ggt gtt ttt				680
Asn Asp Asp Asp Phe Tyr Glu Leu Val Gly Asp Asp Asp Gly Val Phe	195	200	205	
ggg tgc atg agc ctt atc gct tgc cat gac act tgc cc taaagaatta				728
Gly Cys Met Ser Leu Ile Ala Cys His Asp Thr Cys	210	215	220	
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<213> Helicobacter pylori

<400> 278

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His Gln Asp Pro Asp Leu Ser Phe Asp Phe Val Cys Arg Ala Gly Ile	50	55	60	



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aac gcc ggg ttt tta gcc tta aat tta aaa tca tgg cgt aaa gaa aat							697								
Asn Ala Gly Phe Leu Ala Leu Asn Leu Lys Ser Trp Arg Lys Glu Asn															
			95			100	105								
							110								



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Pro	Asn	Leu	Glu	Glu 85	Ala	Gln	Ile	Leu	Phe 90	Asp	Asn	Tyr	Phe	Asn 95	Ala	
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Asn	Asp	Gln 130	Asp	Ala	Leu	Cys 135	Phe	Val	Cys	Arg	Gly 140	Arg	Ile	Leu	Glu	
Leu 145	Pro	Tyr	Pro	Tyr	Asn 150	Ala	His	Pro	Ser	Phe 155	Leu	Asp	Thr	Leu	Ser 160	
Phe	Pro	Ser	Ile	Lys 165	Glu	Ala	Arg	Met	Leu 170	His	Phe	Trp	Gly	Asp 175	Lys	
Pro	Trp	Lys	Leu 180	Leu	Ser	Val	Ile	Gly 185	Ala	Lys	Lys	Trp	His 190	Glu	Ala	
Leu	Ile	Gln 195	Thr	Pro	Phe	Lys	Asp 200	Ala	Tyr	Phe	Asn	Ala 205	Ser	Phe	Leu	
Asp	His 210	Leu	Phe	Glu	Ser	Leu 215	Gln	Asn	Lys	Asp	Asn 220	Glu	Ile	Lys	Arg	
Arg 225	Asp	Glu	Arg	Ile	Ile 230	Ala	Leu	Gln	Ala 235	Arg	Asp	Lys	Ile	Leu	240	
Ser	Phe	Ser	Asp	Lys 245	Arg	His	Ser	Phe	Glu 250	Ser	Leu	Leu	Pro	Lys 255	Leu	
Ser	Ser	Lys	Leu 260	Leu	Ile	Glu	Phe	Leu 265	Leu	Phe	Lys	Ala	Lys 270	Gln	Lys	
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<211> 1198
<212> DNA
<213> Helicobacter pylori
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<220>  
<221> CDS  
<222> (51)...(1145)
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Met Asp  
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cct ttt tta agg gat cat tat ggg aat cct agc tcg ttg cac cag ttt 104  
Pro Phe Leu Arg Asp His Tyr Gly Asn Pro Ser Ser Leu His Gln Phe  
5 10 15

ggc aca gaa acc cac cca gcc att gca gaa gcg cta gat aag ctt tat 152  
Gly Thr Glu Thr His Pro Ala Ile Ala Glu Ala Leu Asp Lys Leu Tyr  
20 25 30

aag ggc att aac gct agg gat ata gat gat gtg atc atc act tct tgt 200  
Lys Gly Ile Asn Ala Arg Asp Ile Asp Asp Val Ile Ile Thr Ser Cys  
35 40 45 50

gcg aca gaa agc aat aat tgg gtt tta aag ggc gtg tat ttt gat gaa 248  
Ala Thr Glu Ser Asn Asn Trp Val Leu Lys Gly Val Tyr Phe Asp Glu  
55 60 65

tgc ttg aaa aaa ggc aaa aac cat att gta acc acg gtt gca gag cat	296
Cys Leu Lys Lys Gly Lys Asn His Ile Val Thr Thr Val Ala Glu His	
70 75 80	
ccg gcg gtg cga tcc act tgc aat ttt tta gaa agc ttg ggg gtg gag	344
Pro Ala Val Arg Ser Thr Cys Asn Phe Leu Glu Ser Leu Gly Val Glu	
85 90 95	
gtt act tac ttg ccc att aat gag cat ggg agc atc acc gca gag caa	392
Val Thr Tyr Leu Pro Ile Asn Glu His Gly Ser Ile Thr Ala Glu Gln	
100 105 110	
gtc aaa gaa gcg atc aca gaa aaa acc gct cta gtg agc gtg atg tgg	440
Val Lys Glu Ala Ile Thr Glu Lys Thr Ala Leu Val Ser Val Met Trp	
115 120 125 130	
gcg aat aat gaa acc ggt ctc att ttc cct att gaa gaa att ggg gct	488
Ala Asn Asn Glu Thr Gly Leu Ile Phe Pro Ile Glu Glu Ile Gly Ala	
135 140 145	
att tgt aaa gaa aag ggc gtg ttg ttc cat acc gat gcc gtg caa gcg	536
Ile Cys Lys Glu Lys Gly Val Leu Phe His Thr Asp Ala Val Gln Ala	
150 155 160	
att ggt aaa atc cct gta gat gtg tta aaa gcg aat gca gat ttc ctt	584
Ile Gly Lys Ile Pro Val Asp Val Leu Lys Ala Asn Ala Asp Phe Leu	
165 170 175	
tct ttt agc gcg cac aag ttt cat ggg cct aaa ggc att ggg ggg ttg	632
Ser Phe Ser Ala His Lys Phe His Gly Pro Lys Gly Ile Gly Gly Leu	
180 185 190	
tat att aga agt ggg gtg gga ttg acc cct ctt ttt cat ggc ggg gag	680
Tyr Ile Arg Ser Gly Val Gly Leu Thr Pro Leu Phe His Gly Gly Glu	
195 200 205 210	
cat atg aat ggc agg cgc agc ggg act ttg aat gtg cct tat att gtg	728
His Met Asn Gly Arg Arg Ser Gly Thr Leu Asn Val Pro Tyr Ile Val	
215 220 225	
gga atg ggc gaa gcg atg aaa tta gcc gta gag cat tta gac tat gaa	776
Gly Met Gly Glu Ala Met Lys Leu Ala Val Glu His Leu Asp Tyr Glu	
230 235 240	
aaa gaa gtg gtg ggg aaa ttg cgc gac aaa tta gaa gaa gcg ctt ttg	824
Lys Glu Val Val Gly Lys Leu Arg Asp Lys Leu Glu Glu Ala Leu Leu	
245 250 255	
aaa atc cct gat gtg atg gtg gtg ggc gat aga atc cat cgt gtg cct	872
Lys Ile Pro Asp Val Met Val Val Gly Asp Arg Ile His Arg Val Pro	
260 265 270	
aac acg act tta gtc agc gtg aga ggg att gaa gga gag gcc atg ctg	920
Asn Thr Thr Leu Val Ser Val Arg Gly Ile Glu Gly Glu Ala Met Leu	
275 280 285 290	
tgg gat tta aac cgc tct aat atc gcc gct tcc aca ggg agc gcg tgc	968
Trp Asp Leu Asn Arg Ser Asn Ile Ala Ala Ser Thr Gly Ser Ala Cys	

295	300	305	
gcg agt gag gat tta gag gct aat ccg gtg atg gta gcg att gga gcg			1016
Ala Ser Glu Asp Leu Glu Ala Asn Pro Val Met Val Ala Ile Gly Ala			
310	315	320	
agt aag gaa ttg gct cat acc gct atc agg ctt tca ttg agc cgt ttt			1064
Ser Lys Glu Leu Ala His Thr Ala Ile Arg Leu Ser Leu Ser Arg Phe			
325	330	335	
aac acg gaa gct gaa att gac aaa acg att gaa gtt ttc tct caa gcg			1112
Asn Thr Glu Ala Glu Ile Asp Lys Thr Ile Glu Val Phe Ser Gln Ala			
340	345	350	
gct gta agg ttg aga aat att tca agc tct tat taaaaagaat ataaaggaat			1165
Ala Val Arg Leu Arg Asn Ile Ser Ser Ser Tyr			
355	360	365	
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20 25 30			
Leu Tyr Lys Gly Ile Asn Ala Arg Asp Ile Asp Asp Val Ile Ile Thr			
35 40 45			
Ser Cys Ala Thr Glu Ser Asn Asn Trp Val Leu Lys Gly Val Tyr Phe			
50 55 60			
Asp Glu Cys Leu Lys Lys Gly Lys Asn His Ile Val Thr Thr Val Ala			
65 70 75 80			
Glu His Pro Ala Val Arg Ser Thr Cys Asn Phe Leu Glu Ser Leu Gly			
85 90 95			
Val Glu Val Thr Tyr Leu Pro Ile Asn Glu His Gly Ser Ile Thr Ala			
100 105 110			
Glu Gln Val Lys Glu Ala Ile Thr Glu Lys Thr Ala Leu Val Ser Val			
115 120 125			
Met Trp Ala Asn Asn Glu Thr Gly Leu Ile Phe Pro Ile Glu Glu Ile			
130 135 140			
Gly Ala Ile Cys Lys Glu Lys Gly Val Leu Phe His Thr Asp Ala Val			
145 150 155 160			
Gln Ala Ile Gly Lys Ile Pro Val Asp Val Leu Lys Ala Asn Ala Asp			
165 170 175			
Phe Leu Ser Phe Ser Ala His Lys Phe His Gly Pro Lys Gly Ile Gly			
180 185 190			
Gly Leu Tyr Ile Arg Ser Gly Val Gly Leu Thr Pro Leu Phe His Gly			
195 200 205			
Gly Glu His Met Asn Gly Arg Arg Ser Gly Thr Leu Asn Val Pro Tyr			
210 215 220			
Ile Val Gly Met Gly Glu Ala Met Lys Leu Ala Val Glu His Leu Asp			
225 230 235 240			
Tyr Glu Lys Glu Val Val Gly Lys Leu Arg Asp Lys Leu Glu Glu Ala			
245 250 255			
Leu Leu Lys Ile Pro Asp Val Met Val Val Gly Asp Arg Ile His Arg			





gcg cta ggc att ttg ctt tta atg gag caa ttc aaa ttc ctt caa aac Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu Gln Asn 135 140 145	488
caa aat ttg ggg gtg ttt gtc ttg ctc gct att ggg ata ctc atc att Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu Ile Ile 150 155 160	536
tat ctt ttt cct cta atc act aaa aaa atc ccc tct aat ctg att tgt Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu Ile Cys 165 170 175	584
atc ctt ata gtg agc gcg atc gct tta att ttt gat atg cat gcg ccg Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His Ala Pro 180 185 190	632
aat ttg ggg agc att gag caa ggg gtt tca ggc ttt cat ttc atc att Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe Ile Ile 195 200 205 210	680
atc ccc aaa aat ttg gat ttt aaa ata atg ata gag ttg ttg cct tac Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu Pro Tyr 215 220 225	728
gct ctt tct tta gca cta gtg gga acg ata gaa agc tta ttg acg gct Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu Thr Ala 230 235 240	776
aaa act tta gat gtg att tta aaa gac ggc gtg agc gat aaa aat aaa Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys Asn Lys 245 250 255	824
gaa act aaa gcg caa ggc ttg ggg aat atc atc tca ggg ctt ttg ggg Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu Leu Gly 260 265 270	872
gga atg aca ggg tgc gct tta gtg ggg cag tct atc att aac gca aaa Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn Ala Lys 275 280 285 290	920
tcc ggg gct aaa aca agg ctt tct act ttt ttt gcc ggc ttt tct tta Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe Ser Leu 295 300 305	968
atg gtg ctc ata tta gtg ttt aat gaa tat gtg gtt aag atc ccc att Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile Pro Ile 310 315 320	1016
gtg gcg gtt gtg gcg gta atg gtg atg att tct ttc acc act ttt aat Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr Phe Asn 325 330 335	1064
ttc caa tcc att att aac att aaa aaa atc aag ctc tat gac acg ctc Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp Thr Leu 340 345 350	1112
aac atg ctc tta gtc gtg gcg gtg gtt tta tac acg cat aat tta gcg Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn Leu Ala	1160

355	360	365	370	
ata ggg gtt gtg gtg ggg gtt tta gtc aat gcg tta tgg atc aaa tct				1208
Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile Lys Ser				
375	380	385		
aaa ggg att gca tgaaatttta ttttaaaaag ttgggtagct agagatatgg				1260
Lys Gly Ile Ala				
390				
ctccagatgt agg				1273
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Asn Ile Gln Lys Asp Leu Leu Ser Gly Phe Val Val Gly Leu Ser Val				
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Ile Pro Glu Thr Ala Gly Phe Ala Ile Met Val Gly Leu Asp Val Gly				
35 40 45				
Val Ala Phe Tyr Thr Thr Phe Tyr Met Ala Phe Val Leu Ser Leu Phe				
50 55 60				
Gly Ala Arg Lys Ala Met Ile Ser Ala Ala Ala Gly Ser Val Ala Leu				
65 70 75 80				
Ile Leu Val Gly Val Val Lys Asn Tyr Gly Leu Glu Tyr Ala Gly Val				
85 90 95				
Ala Thr Leu Met Ala Gly Val Leu Gln Ile Leu Leu Gly Tyr Leu Lys				
100 105 110				
Ile Gly Asn Leu Leu Arg Phe Ile Pro Gln Ser Val Met Tyr Gly Phe				
115 120 125				
Val Asn Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu				
130 135 140				
Gln Asn Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu				
145 150 155 160				
Ile Ile Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu				
165 170 175				
Ile Cys Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His				
180 185 190				
Ala Pro Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe				
195 200 205				
Ile Ile Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu				
210 215 220				
Pro Tyr Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu				
225 230 235 240				
Thr Ala Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys				
245 250 255				
Asn Lys Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu				
260 265 270				
Leu Gly Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn				
275 280 285				
Ala Lys Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe				
290 295 300				
Ser Leu Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile				
305 310 315 320				
Pro Ile Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr				

325 330 335  
 Phe Asn Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp  
 340 345 350  
 Thr Leu Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn  
 355 360 365  
 Leu Ala Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile  
 370 375 380  
 Lys Ser Lys Gly Ile Ala  
 385 390

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 <213> Helicobacter pylori

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 <222> (386)...(964)

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 gaaaaaagaa tgcttgatag aaagcgaaat tcaaatacgtt aagactaagg gcgataaaat 180  
 cttagacacc cctttaaata agatcggcgg taaggggcta ttcactaagg aattagaaga 240  
 attgctttta aagggcgcaa ttgatttggc ggtgcattct ttaaaagacg tgccggtcgt 300  
 gtttgaaaag gggtttagact tggcatgcat caccaaaaagg gctgatgtga gggacacttt 360  
 ttttagcgtg aaattccctg atttg atg agt ttg cct aaa ggg gca aag gtt 412  
 Met Ser Leu Pro Lys Gly Ala Lys Val  
 1 5  
 ggc acg act tct tta agg cgc tct atg cag atc aaa tta aag cgc cag 460  
 Gly Thr Thr Ser Leu Arg Arg Ser Met Gln Ile Lys Leu Lys Arg Gln  
 10 15 20 25  
 gat ttg gac aca gaa agc ttg aga ggg aat gtc caa acc cgt ttg aaa 508  
 Asp Leu Asp Thr Glu Ser Leu Arg Gly Asn Val Gln Thr Arg Leu Lys  
 30 35 40  
 aag ctt gaa tgc gga gaa ttt gac gct atc att tta gct gaa gcc ggg 556  
 Lys Leu Glu Cys Gly Glu Phe Asp Ala Ile Ile Leu Ala Glu Ala Gly  
 45 50 55  
 ttg tgc cgc cta gaa att caa gga gcg aaa tac cgc aag gct ttt agc 604  
 Leu Cys Arg Leu Glu Ile Gln Gly Ala Lys Tyr Arg Lys Ala Phe Ser  
 60 65 70  
 gta gaa gaa atg att cct agc atg ggt cag ggg gct tta ggg gta gaa 652  
 Val Glu Glu Met Ile Pro Ser Met Gly Gln Gly Ala Leu Gly Val Glu  
 75 80 85  
 atg ctc aaa aac cac aag cat ttt gcc acg ctt caa aaa ctc aac gac 700  
 Met Leu Lys Asn His Lys His Phe Ala Thr Leu Gln Lys Leu Asn Asp  
 90 95 100 105  
 gag aaa agc gcg ttt tgc tgc cgt tta gaa agg gag ttt atc aag ggg 748  
 Glu Lys Ser Ala Phe Cys Cys Arg Leu Glu Arg Glu Phe Ile Lys Gly  
 110 115 120  
 ctt aat gga ggg tgt cag atc cct ata ggc gtg cat gcg agt tta atg 796



[illegible]

gct gta acc atc ttt cat gat aaa ttc cct cgc tct cac cag ccc aaa 104  
Ala Val Thr Ile Phe His Asp Lys Phe Pro Arg Ser His Gln Pro Lys  
5 10 15

tct tgg gcg gat ttc atc acg gaa ttt cgt gtg gat ttg ata gag atg 152  
Ser Trp Ala Asp Phe Ile Thr Glu Phe Arg Val Asp Leu Ile Glu Met  
20 25 30

gac ggg caa ttg ctt gta act ttt aat gaa att agc ggc aat ttc ggt 200  
Asp Gly Gln Leu Leu Val Thr Phe Asn Glu Ile Ser Gly Asn Phe Gly  
35 40 45 50

gat att ttc ttc taaagtgggg cttaaaacaa aatcattgtc ttttcgggtct 252  
Asp Ile Phe Phe

ttaaaaacca ata 265

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<210> 290
<211> 54
<212> PRT
<213> Helicobacter pylori
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[illegible]

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<210> 291
<211> 1350
<212> DNA
<213> Helicobacter pylori
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<220>  
<221> CDS  
<222> (73) ... (1305)
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ggataaatatt tt atg gca gat gtc gtt gtg ggg atc cag tgg gga gat gag      111
      Met Ala Asp Val Val Gly Ile Gln Trp Gly Asp Glu
            1             5             10

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ggg aag gga aaa att gtt gat agg atc gct aaa gat tat gac ttt gtg 159  
Gly Lys Gly Lys Ile Val Asp Arg Ile Ala Lys Asp Tyr Asp Phe Val

15	20	25	
gtg cgc tat cag ggc ggg cat aat gct ggg cat acc att gtg cat aag			207
Val Arg Tyr Gln Gly Gly His Asn Ala Gly His Thr Ile Val His Lys			
30	35	40	45
ggg gtt aag cat tct ttg cat tta atg cct tca ggg gtt tta tac ccc			255
Gly Val Lys His Ser Leu His Leu Met Pro Ser Gly Val Leu Tyr Pro			
	50	55	60
aaa tgc aag aac atc att tct agc gcg gtg gtc gtg agc gtt aag gat			303
Lys Cys Lys Asn Ile Ile Ser Ser Ala Val Val Val Ser Val Lys Asp			
	65	70	75
ttg tgc gaa gaa atc agc gcg ttt gag gat tta gaa aat cgt ttg ttt			351
Leu Cys Glu Glu Ile Ser Ala Phe Glu Asp Leu Glu Asn Arg Leu Phe			
	80	85	90
gtc agc gac aga gcc cat gtg atc ttg ccc tat cat gcc aaa aaa gac			399
Val Ser Asp Arg Ala His Val Ile Leu Pro Tyr His Ala Lys Lys Asp			
	95	100	105
gct ttt aaa gaa aaa tct caa aac atc ggc acg act aaa aaa ggc ata			447
Ala Phe Lys Glu Lys Ser Gln Asn Ile Gly Thr Thr Lys Lys Gly Ile			
110	115	120	125
ggc cct tgc tat gag gat aaa atg gcc agg agc ggg ata aga atg ggg			495
Gly Pro Cys Tyr Glu Asp Lys Met Ala Arg Ser Gly Ile Arg Met Gly			
	130	135	140
gat tta tta gac gat aaa atc tta gaa gaa aag cta aac gct cat ttc			543
Asp Leu Leu Asp Asp Lys Ile Leu Glu Glu Lys Leu Asn Ala His Phe			
	145	150	155
aaa gcc att gag cct ttt aaa aaa gcg tat gat ttg ggc gag aat tac			591
Lys Ala Ile Glu Pro Phe Lys Lys Ala Tyr Asp Leu Gly Glu Asn Tyr			
	160	165	170
gaa aaa gat ttg atg ggg tat ttt aaa act tac gct cca aaa att tgc			639
Glu Lys Asp Leu Met Gly Tyr Phe Lys Thr Tyr Ala Pro Lys Ile Cys			
	175	180	185
ccc ttt atc aaa gac acg aca agc atg ctg ata gaa gcg aat caa aag			687
Pro Phe Ile Lys Asp Thr Thr Ser Met Leu Ile Glu Ala Asn Gln Lys			
190	195	200	205
ggt gaa aaa atc cta tta gaa ggg gca caa ggc acg ctt tta gac att			735
Gly Glu Lys Ile Leu Leu Glu Gly Ala Gln Gly Thr Leu Leu Asp Ile			
	210	215	220
gat tta ggg act tac cct ttt gta aca agc tct aac acc acg agc gct			783
Asp Leu Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Thr Thr Ser Ala			
	225	230	235
agc gca tgc gtg agc acc ggc tta aac cct aaa gcg atc aat gaa gtc			831
Ser Ala Cys Val Ser Thr Gly Leu Asn Pro Lys Ala Ile Asn Glu Val			
	240	245	250
ata ggt atc aca aaa gcc tac tcc act cgt gtg ggt aat ggg cct ttc			879

Ile Gly Ile Thr Lys Ala Tyr Ser Thr Arg Val Gly Asn Gly Pro Phe	
255 260 265	
cct agc gaa gac act aca ccc atg ggc gat cat tta agg act aag ggt	927
Pro Ser Glu Asp Thr Thr Pro Met Gly Asp His Leu Arg Thr Lys Gly	
270 275 280 285	
gcg gag ttt ggc acg aca acc aag cgc cca agg cgt tgc ggg tgg ctg	975
Ala Glu Phe Gly Thr Thr Thr Lys Arg Pro Arg Arg Cys Gly Trp Leu	
290 295 300	
gat ttg gtg gct ttg aaa tac gct tgc gct ttg aat ggt tgc acg caa	1023
Asp Leu Val Ala Leu Lys Tyr Ala Cys Ala Leu Asn Gly Cys Thr Gln	
305 310 315	
tta gcc tta atg aaa tta gac gtt tta gac ggg att gat gcg att aag	1071
Leu Ala Leu Met Lys Leu Asp Val Leu Asp Gly Ile Asp Ala Ile Lys	
320 325 330	
gtg tgc gtg gct tat gaa aga aag ggc gaa aga ttg gag att ttc cct	1119
Val Cys Val Ala Tyr Glu Arg Lys Gly Glu Arg Leu Glu Ile Phe Pro	
335 340 345	
agc gat ttg aaa gat tgc gtg ccg atc tat caa act ttt aaa ggt tgg	1167
Ser Asp Leu Lys Asp Cys Val Pro Ile Tyr Gln Thr Phe Lys Gly Trp	
350 355 360 365	
gaa aaa agc gtg ggc gtg aga aaa tta gac gat tta gag cca aac gtt	1215
Glu Lys Ser Val Gly Val Arg Lys Leu Asp Asp Leu Glu Pro Asn Val	
370 375 380	
aga gag tat atc cgt ttt att gaa aaa gaa gtg ggg gta aaa atc cgc	1263
Arg Glu Tyr Ile Arg Phe Ile Glu Lys Glu Val Gly Val Lys Ile Arg	
385 390 395	
ctt att tct aca agc cct gaa aga gaa gac acg att ttt cta	1305
Leu Ile Ser Thr Ser Pro Glu Arg Glu Asp Thr Ile Phe Leu	
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 <212> PRT  
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<400> 292

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35 40 45	
His Ser Leu His Leu Met Pro Ser Gly Val Leu Tyr Pro Lys Cys Lys	
50 55 60	
Asn Ile Ile Ser Ser Ala Val Val Val Ser Val Lys Asp Leu Cys Glu	
65 70 75 80	
Glu Ile Ser Ala Phe Glu Asp Leu Glu Asn Arg Leu Phe Val Ser Asp	
85 90 95	

Arg Ala His Val Ile Leu Pro Tyr His Ala Lys Lys Asp Ala Phe Lys  
 100 105 110  
 Glu Lys Ser Gln Asn Ile Gly Thr Lys Lys Gly Ile Gly Pro Cys  
 115 120 125  
 Tyr Glu Asp Lys Met Ala Arg Ser Gly Ile Arg Met Gly Asp Leu Leu  
 130 135 140  
 Asp Asp Lys Ile Leu Glu Glu Lys Leu Asn Ala His Phe Lys Ala Ile  
 145 150 155 160  
 Glu Pro Phe Lys Lys Ala Tyr Asp Leu Gly Glu Asn Tyr Glu Lys Asp  
 165 170 175  
 Leu Met Gly Tyr Phe Lys Thr Tyr Ala Pro Lys Ile Cys Pro Phe Ile  
 180 185 190  
 Lys Asp Thr Thr Ser Met Leu Ile Glu Ala Asn Gln Lys Gly Glu Lys  
 195 200 205  
 Ile Leu Leu Glu Gly Ala Gln Gly Thr Leu Leu Asp Ile Asp Leu Gly  
 210 215 220  
 Thr Tyr Pro Phe Val Thr Ser Ser Asn Thr Thr Ser Ala Ser Ala Cys  
 225 230 235 240  
 Val Ser Thr Gly Leu Asn Pro Lys Ala Ile Asn Glu Val Ile Gly Ile  
 245 250 255  
 Thr Lys Ala Tyr Ser Thr Arg Val Gly Asn Gly Pro Phe Pro Ser Glu  
 260 265 270  
 Asp Thr Thr Pro Met Gly Asp His Leu Arg Thr Lys Gly Ala Glu Phe  
 275 280 285  
 Gly Thr Thr Thr Lys Arg Pro Arg Arg Cys Gly Trp Leu Asp Leu Val  
 290 295 300  
 Ala Leu Lys Tyr Ala Cys Ala Leu Asn Gly Cys Thr Gln Leu Ala Leu  
 305 310 315 320  
 Met Lys Leu Asp Val Leu Asp Gly Ile Asp Ala Ile Lys Val Cys Val  
 325 330 335  
 Ala Tyr Glu Arg Lys Gly Glu Arg Leu Glu Ile Phe Pro Ser Asp Leu  
 340 345 350  
 Lys Asp Cys Val Pro Ile Tyr Gln Thr Phe Lys Gly Trp Glu Lys Ser  
 355 360 365  
 Val Gly Val Arg Lys Leu Asp Asp Leu Glu Pro Asn Val Arg Glu Tyr  
 370 375 380  
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 385 390 395 400  
 Thr Ser Pro Glu Arg Glu Asp Thr Ile Phe Leu  
 405 410

<210> 293  
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 <212> DNA  
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 <222> (51)...(1310)

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 Val Asp  
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 Val Leu Ser Val Ser Glu Ile Asn Ala Gln Ile Lys Ala Leu Leu Glu  
 5 10 15



gcg act ttt ttg caa gtt agg gtt caa ggg gaa gtg agt aat ttg act Ala Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr 20 25 30	152
atc cat aag gtg agc ggc cat gcg tat ttt tgc ctc aaa gac agc cag Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln 35 40 45 50	200
tcg gtt att aaa tgc gtg ctg ttt aaa ggg aac gct aac agg ctc aaa Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys 55 60 65	248
ttc gct tta aaa gaa ggg cag gaa gtg gtt gtt ttt ggg ggt att agc Phe Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly Ile Ser 70 75 80	296
gtg tat gtc cca agg ggg gat tat caa atc aat tgc ttt gaa ata gag Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu 85 90 95	344
cct aag gat ata ggt tca tta act tta gct tta gag caa ttg aaa gaa Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu 100 105 110	392
aaa tta cgc ctt aaa ggc tat ttt gat gaa gaa aat aaa tta ccc aaa Lys Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys 115 120 125 130	440
ccg cat ttt cct aaa cga gtg gca gtc atc act tct caa aat tca gcc Pro His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala 135 140 145	488
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Gly Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln	
275 280 285 290	
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Lys Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser	
295 300 305	
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Phe Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys	
310 315 320	
atc gcc cta gaa aat aaa act cta gaa ttt tta cgc ttt aaa aaa acg	1064
Ile Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr	
325 330 335	
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Leu Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln	
340 345 350	
act aaa aca gag cga ttg aac agg cta gaa aac gcc ctt aaa ctc gct	1160
Thr Lys Thr Glu Arg Leu Asn Arg Leu Glu Asn Ala Leu Lys Leu Ala	
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Asn Gln Ala Ile Glu Leu Glu Ala Leu Lys Arg Gly Asp Lys Ile Glu	
390 395 400	
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Leu Ser Asn Glu Lys Thr Arg Ala Ser Ala Glu Ile Leu Ser Val Asp	
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Lys Gly Leu Lys Lys Ala Phe Lys Glu Arg Phe Cys Ser Gln Val Tyr																			
5					10					15									
atc tct ttt aat gtg gat cac aat ctt tta tcc act caa gtc ata agg	152																		
Ile Ser Phe Asn Val Asp His Asn Leu Leu Ser Thr Gln Val Ile Arg																			
20					25					30									
atc aaa aac gat cgc att aaa gag aaa ttt ttt aaa act ttt gag act	200																		
Ile Lys Asn Asp Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe Glu Thr																			
35					40					45					50				
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Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu Lys Ile																			
55					60					65									
gcc aga act tat agc caa aaa tac ccc tac act tat ttt agc gcg atg	296																		
Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser Ala Met																			
70					75					80									
agt aaa gct aaa gag gtt tta tgc gaa aag cag gcg ttt gaa caa atc	344																		
Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu Gln Ile																			
85					90					95									
aaa caa gaa aat caa gat tat cat gct tgt gaa gtc aat caa aag tat	392																		
Lys Gln Glu Asn Gln Asp Tyr His Ala Cys Glu Val Asn Gln Lys Tyr																			
100					105					110									
tgc gtt tat gtg gaa tct aag gat ttt tta aag gat ttt aag cgt ttt	440																		
Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys Arg Phe																			
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165					170					175									
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Phe Leu Ala Lys Ser Val Phe Leu Glu Glu Gln Pro Glu Glu Phe Ile																			
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215					220					225									

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gct tat agt ttg att gaa ggc atg acg aat atc ccc tta att gca gat Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile Ala Asp 245 250 255	824
gtt ttg caa gag gga ttg cgt ggc gtc tat cat tct aga gag ata gac Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu Ile Asp 260 265 270	872
ttt gta gaa aaa gtg gtt gtt tta gac agc tgt caa atc cac caa aaa Phe Val Glu Lys Val Val Val Leu Asp Ser Cys Gln Ile His Gln Lys 275 280 285 290	920
gcg tta atg cat ttg caa gaa act ttg atg ata gaa gtg gat agg ctt Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp Arg Leu 295 300 305	968
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Glu Thr Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu 50 55 60	
Lys Ile Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser 65 70 75 80	
Ala Met Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu 85 90 95	
Gln Ile Lys Gln Glu Asn Gln Asp Tyr His Ala Cys Glu Val Asn Gln 100 105 110	
Lys Tyr Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys 115 120 125	
Arg Phe Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu 130 135 140	
Ile Tyr Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr 145 150 155 160	
Leu Leu Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys 165 170 175	



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Ser	Leu	Ser 100	Asp	Asn	Val	Lys	Leu 105	Gln	Glu	Asp	Gly	Ile 110	Val	Phe	Lys	
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Ser	His 115	Ile	Asp	Gly	Ser	Lys 120	His	Leu	Phe	Thr	Pro 125	Ala	Lys	Val	Leu	
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Asp 130	Ile	Gln	Tyr	Ser	Leu 135	Asn	Ser	Asp	Ile	Met 140	Met	Val	Leu	Asp	Asp 145	
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Arg	Ser	Ala 165	Lys	Trp	Ala	Asn	Met	Ser 170	Leu	Glu	Tyr	His	Lys 175	Glu	Lys	
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Gly 210	Tyr	Ala	Ile	Gly 215	Gly	Leu	Ala	Val	Gly 220	Glu	Ser	Ala	Asp	Glu	Met 225	
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Leu	Glu	Thr	Ile 230	Ala	His	Thr	Ala	Pro	Leu 235	Leu	Pro	Lys	Asp	Lys 240	Pro	
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Arg	Tyr	Leu 245	Met	Gly	Val	Gly	Thr	Pro 250	Glu	Asn	Ile	Leu	Asp 255	Ala	Ile	
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Ser	Leu 260	Gly	Val	Asp	Met	Phe 265	Asp	Cys	Val	Met	Pro 270	Thr	Arg	Asn	Ala	
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Arg 275	Asn	Ala	Thr	Leu	Phe 280	Thr	His	Ser	Gly	Lys	Ile 285	Ser	Ile	Lys	Asn	
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Ala 290	Pro	Tyr	Lys	Leu	Asp 295	Asn	Thr	Pro	Ile	Glu	Glu	Asn	Cys	Ala	Cys 305	
tat	gct	tgc	aaa	cgc	tat	tct	aaa	gcc	tat	ttg	cac	cat	tta	ttt	agg	1020
Tyr	Ala	Cys	Lys	Arg 310	Tyr	Ser	Lys	Ala	Tyr 315	Leu	His	His	Leu	Phe	Arg	
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Ala	Lys	Glu	Leu 325	Thr	Tyr	Ala	Arg	Leu 330	Ala	Ser	Leu	His	Asn 335	Leu	His	

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 340 345 350  
 cgg ttt ttg agt ttt aaa aaa gaa ttt ttg gag aaa tac aac tcc cgc 1164  
 Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser Arg  
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 <213> Helicobacter pylori

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 Gly Thr Gln Gly Cys Ile Lys Ser Leu Asp Ala Thr Asp Ala Gln Glu  
 35 40 45  
 Ile Leu Gly Ala Lys Leu Ile Leu Ala Asn Thr Tyr His Met Tyr Leu  
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 Arg Pro Gly Glu Lys Val Val Glu Glu Leu Gly Gly Leu His Arg Phe  
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 Ala Gln Phe Tyr Gly Ser Phe Leu Thr Asp Ser Gly Gly Phe Gln Ala  
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 Phe Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe  
 100 105 110  
 Lys Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val  
 115 120 125  
 Leu Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp  
 130 135 140  
 Asp Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile  
 145 150 155 160  
 Lys Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu  
 165 170 175  
 Lys Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr  
 180 185 190  
 His Leu Lys Met Arg Ser Leu Ser Val Gly Leu Thr His Glu Gly Phe  
 195 200 205  
 Asp Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu  
 210 215 220  
 Met Leu Glu Thr Ile Ala His Thr Ala Pro Leu Leu Pro Lys Asp Lys  
 225 230 235 240  
 Pro Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala  
 245 250 255  
 Ile Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn  
 260 265 270  
 Ala Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys  
 275 280 285  
 Asn Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala  
 290 295 300



Cys Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe  
 305 310 315 320  
 Arg Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu  
 325 330 335  
 His Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu  
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 Arg Ser His  
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 Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg Thr Asn Leu Phe Asp Thr  
 5 10 15  
 caa gtg atg agc gag aat ttg aag gac ttt agc acg acc tta gaa gaa 152  
 Gln Val Met Ser Glu Asn Leu Lys Asp Phe Ser Thr Thr Leu Glu Glu  
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 Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr Asn Gly  
 35 40 45 50  
 gcc gat agc gcg gta agg agt tac gct aaa aaa atg gca cgg ttg gat 248  
 Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg Leu Asp  
 55 60 65  
 aag gaa gtg cta ttt act ggt tgc ggg gtg aaa acc caa ggc aaa gag 296  
 Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly Lys Glu  
 70 75 80  
 ctt ttt gaa aaa ggg ttt tta aag ggc gtt ttt ggg cat gac aat aaa 344  
 Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp Asn Lys  
 85 90 95  
 gaa aag att aac gcg ctt tta caa gaa aaa aag cgt ttt ttt ata gat 392  
 Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe Ile Asp  
 100 105 110  
 gac aat tta gaa aac aag cac tta gac acc acg atg gtg agc gag ttt 440  
 Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser Glu Phe  
 115 120 125 130  
 gtg gga aaa act agg gcg ttt att aag atc caa gaa ggc tgt gat ttt 488  
 Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys Asp Phe



Val Glu Val Gln Lys Asp Gly Glu Phe Lys Ala Leu Asp Gln Phe Phe  
 375 380 385

aac ccc att aaa atc aaa agc gat aag cct cta agg gct agt ttt tta 1256  
 Asn Pro Ile Lys Ile Lys Ser Asp Lys Pro Leu Arg Ala Ser Phe Leu  
 390 395 400

gaa atc aaa gag tat gaa att aag gag agg gaa aat cat gcc gtt ttc 1304  
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 405 410 415

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 <212> PRT  
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 Glu Glu Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr  
 35 40 45  
 Asn Gly Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg  
 50 55 60  
 Leu Asp Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly  
 65 70 75 80  
 Lys Glu Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp  
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 Asn Lys Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe  
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 Asp Phe Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val Arg Gly Arg Ala  
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 Arg Ser Phe Glu Glu Arg Lys Ile Leu Glu Gln Val Gly Leu Leu Cys  
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 Ser Lys Gly Val Gln Glu Val Val Leu Thr Gly Thr Asn Val Gly Ser  
 180 185 190  
 Tyr Gly Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu Ile Lys Lys Leu  
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 Ser Gln Ile Ala Gly Leu Lys Arg Ile Arg Ile Gly Ser Leu Glu Pro  
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 Asn Gln Ile Asn Asp Glu Phe Leu Glu Leu Leu Glu Glu Asp Phe Leu  
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 Glu Arg Met Asn Arg Arg Asn Arg Thr Lys Ser Asp Arg Glu Leu Leu  
 260 265 270  
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 275 280 285  
 Gly His Pro Gly Glu Ser Gly Ser Val Phe Glu Lys Ala Phe Lys Asn  
 290 295 300  
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 305 310 315 320

Arg Lys Asp Thr Pro Ser Ser Leu Met Thr Asp Ser Val Ser Leu Glu  
325 330 335  
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340 345 350  
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355 360 365  
Ala Leu Val Glu Val Gln Lys Asp Gly Glu Phe Lys Ala Leu Asp Gln  
370 375 380  
Phe Phe Asn Pro Ile Lys Ile Lys Ser Asp Lys Pro Leu Arg Ala Ser  
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35 40 45 50

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ggt ttt gta gtg tta ctt tat gaa atc att tcg ttt att tat tac aaa 296  
Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr Tyr Lys  
70 75 80

aga tcg tta gtg tat ttg atc ctt ggc gtg gcg ata ggg gcg ttg tgt 344  
Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala Leu Cys  
85 90 95

ttg ctc ttt gtt ttt tat tac acg cct tat att tta aac gct caa aaa 392  
Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala Gln Lys  
100 105 110

gcg ggc gaa gcc gcg ctt caa agt gct gaa ttt gcc cgc tcg cac gct 440  
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115                120                125                130
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                135                140                145

ttt ttt tgg cgt ttg ctt gga aaa aat gtg ctt tagtcccttt gatttaatca      541
Phe Phe Trp Arg Leu Leu Gly Lys Asn Val Leu
                150                155

aatgagagag tttttggcta ctatctagga aat      574

<210> 302
<211> 157
<212> PRT
<213> Helicobacter pylori

<400> 302
Met Lys Lys Phe Gly Leu Gly Val Tyr Leu Leu Leu Leu Gly Ile Leu
 1          5          10          15
Gly Gly Ser Leu Ile Ile Leu Gly Ala Ile Val Ala Pro Ile Val Phe
 20          25          30
Lys Ala Ser Ser Val Leu Pro Glu Leu His Leu Thr Pro Phe Glu Ser
 35          40          45
Gly Lys Leu Met Ala Gln Ile Phe Val Arg Phe Asn Tyr Val Leu Gly
 50          55          60
Ala Ile Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr
 65          70          75          80
Tyr Lys Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala
 85          90          95
Leu Cys Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala
100          105          110
Gln Lys Ala Gly Glu Ala Ala Leu Gln Ser Ala Glu Phe Ala Arg Ser
115          120          125
His Ala Gln Ser Glu Trp Leu Phe Lys Glu Leu Phe Val Leu Val Cys
130          135          140
Ala Leu Phe Phe Trp Arg Leu Leu Gly Lys Asn Val Leu
145          150          155

<210> 303
<211> 1780
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(1727)

<400> 303
ataaccggt gtttttgata gacaaatagc aagccgttgc taaaaattaa atg att      56
                                   Met Ile
                                   1

ttt ggg gat ttt aaa tat caa aaa agc gtt aaa aaa ctc aca gcc acc      104
Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr Ala Thr
 5          10          15

aat ctt aat gag ctt aaa aac gcc ctg gat ttc atc tct caa aat agg      152
Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln Asn Arg

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20	25	30	
ggg aat ggg tat ttt gtg ggg tat ctt tta tat gaa gcg cgc tta gcg Gly Asn Gly Tyr Phe Val Gly Tyr Leu Leu Tyr Glu Ala Arg Leu Ala 35 40 45 50			200
ttt tta gat gaa aat ttt caa agc caa acc cct ttt ttg tat ttt gaa Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr Phe Glu 55 60 65			248
caa ttt tta gaa aga aaa aaa tat tct tta gag cct tta aaa gag cat Gln Phe Leu Glu Arg Lys Lys Tyr Ser Leu Glu Pro Leu Lys Glu His 70 75 80			296
gcg ttt tac cct aaa atc cat agt tct tta gat caa aaa act tat ttc Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr Tyr Phe 85 90 95			344
aag cag ttt aaa gcc gtt aaa gag cgt ctc aaa aac ggc gac acc tat Lys Gln Phe Lys Ala Val Lys Glu Arg Leu Lys Asn Gly Asp Thr Tyr 100 105 110			392
caa gtg aat ctc aca atg gat tta ttt tta gac act aaa gcc aaa cca Gln Val Asn Leu Thr Met Asp Leu Phe Leu Asp Thr Lys Ala Lys Pro 115 120 125 130			440
aag cgc gtt ttt aag gag gtg gta cac aac caa aac acg cct ttt aag Lys Arg Val Phe Lys Glu Val Val His Asn Gln Asn Thr Pro Phe Lys 135 140 145			488
gct ttt ata gaa aat gag ttt ggg agc gtt tta agc ttt tcg ccg gaa Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser Pro Glu 150 155 160			536
ttg ttt ttt gaa tta gag ttt tta gat aca gcg att aag att att aca Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile Ile Thr 165 170 175			584
aaa ccc atg aaa ggc acg atc gct cgc tca aaa aac ccc tta ata gat Lys Pro Met Lys Gly Thr Ile Ala Arg Ser Lys Asn Pro Leu Ile Asp 180 185 190			632
gaa aaa aac cga ttg ttt ttg caa aat gat gac aaa aac aga agc gaa Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg Ser Glu 195 200 205 210			680
aat gtg atg att gtg gat tta ttg cgt aac gat ttg agc cgc ttg gcc Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg Leu Ala 215 220 225			728
tta aaa aat agc gtg aaa gtc aat caa ttg ttt gaa atc atc agc ttg Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile Ser Leu 230 235 240			776
cct agc gtg tat caa atg ata agc gag att gaa gcg aaa ttg ccc cta Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Lys Leu Pro Leu 245 250 255			824
aaa acc agc ttg ttt gag att ttt aag gcg ttg ttc cct tgc ggc tct			872







	275		280		285
Ser	Leu	Glu	Lys	Arg	Pro
290				295	
Val	Glu	Glu	Lys	Lys	Ala
305				310	
Lys	Arg	Val	His	Glu	Asn
				325	
Thr	Tyr	Lys	Ser	Lys	Ala
				340	
Ser	Phe	Phe	Val	Met	Pro
				355	
Lys	Ile	Ile	Lys	Lys	Asp
370				375	
His	Lys	Glu	Arg	Leu	Met
385				390	
Asp	Glu	Asn	Leu	Leu	Asp
				405	
Val	Leu	Leu	Asn	Lys	Lys
				420	
Glu	Pro	Leu	Lys	Ser	Leu
				435	
Lys	Arg	Asn	Asp	Phe	Leu
				450	
Gln	Lys	Ala	Arg	Ala	Leu
465				470	
Phe	Tyr	Asn	Gln	Asp	Leu
				485	
Val	Leu	Glu	Ile	His	Asn
				500	
Ala	Leu	Asn	Gly	Thr	Gly
				515	
Gly	His	Ala	Pro	Leu	Lys
				530	
Tyr	Cys	Ile	Asn	Ala	Leu
545				550	

<210> 305  
 <211> 958  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> (51)...(905)

<400> 305

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Met Glu	
1	
tct ttt aga gag ttt atc caa caa ttc aaa aaa aat aag gca gcg gtc	104
Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala Ala Val	
5 10 15	
gtt ggg gct tgg att gtg ctt tta ttg gta att tgc gcg att ttt gcg	152
Val Gly Ala Trp Ile Val Leu Leu Val Ile Cys Ala Ile Phe Ala	
20 25 30	
ccc ctt tta gcc ccg cat gat cct tat gtc caa aac gcg caa gat cgc	200



atc atg gac gct tta gat cct aaa cgc acc tct taaaaggagc ttgcatgatt 925  
 Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser  
 275 280 285

ttagaagtta aagatttaaa aacttatttt ttc 958

<210> 306  
 <211> 285  
 <212> PRT  
 <213> Helicobacter pylori

<400> 306  
 Met Glu Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala  
 1 5 10 15  
 Ala Val Val Gly Ala Trp Ile Val Leu Leu Leu Val Ile Cys Ala Ile  
 20 25 30  
 Phe Ala Pro Leu Leu Ala Pro His Asp Pro Tyr Val Gln Asn Ala Gln  
 35 40 45  
 Asp Arg Leu Leu Lys Pro Ile Trp Glu His Gly Gly Asn Ala Lys Tyr  
 50 55 60  
 Leu Leu Gly Thr Asp Asp Leu Gly Arg Asp Ile Leu Ser Arg Leu Ile  
 65 70 75 80  
 Tyr Gly Ala Arg Ile Ser Leu Thr Ile Gly Ile Val Ser Met Gly Ile  
 85 90 95  
 Ala Val Phe Phe Gly Thr Ile Leu Gly Leu Ile Ala Gly Tyr Phe Gly  
 100 105 110  
 Gly Lys Thr Asp Ala Ile Ile Met Arg Ile Met Asp Ile Met Phe Ala  
 115 120 125  
 Leu Pro Ser Ile Leu Leu Ile Val Ile Val Val Ala Val Leu Gly Pro  
 130 135 140  
 Ser Leu Thr Asn Ala Met Leu Ala Ile Gly Phe Val Gly Ile Pro Gly  
 145 150 155 160  
 Phe Ala Arg Leu Val Arg Ser Ser Val Leu Gly Glu Lys Glu Lys Glu  
 165 170 175  
 Tyr Val Ile Ala Ser Lys Ile Asn Gly Ser Ser His Leu Arg Leu Met  
 180 185 190  
 Cys Lys Val Ile Phe Pro Asn Cys Ile Ile Pro Leu Ile Val Gln Thr  
 195 200 205  
 Thr Met Gly Phe Ala Ser Thr Val Leu Glu Ala Ala Ala Leu Ser Phe  
 210 215 220  
 Leu Gly Leu Gly Ala Gln Pro Pro Lys Pro Glu Trp Gly Ala Met Leu  
 225 230 235 240  
 Met Asn Ser Met Gln Tyr Ile Ala Thr Ala Pro Trp Met Leu Val Phe  
 245 250 255  
 Pro Gly Val Met Ile Phe Leu Thr Val Met Ser Phe Asn Leu Val Gly  
 260 265 270  
 Asp Gly Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser  
 275 280 285

<210> 307  
 <211> 791  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (95)...(727)

<400> 307



<210> 308  
 <211> 211  
 <212> PRT  
 <213> Helicobacter pylori

<400> 308  
 Met Gly Val Asn Tyr Gln Thr Gly Ser Ile Asn Leu Met Thr Asn Ile  
 1 5 10 15  
 His Glu Val Arg Glu Val Thr Asn Tyr Gln Thr Gly Tyr Thr Asn Ile  
 20 25 30  
 Ile Thr Ser Val Asn Ser Val Lys Lys Leu Thr Asn Met Gly Ser Asn  
 35 40 45  
 Gly Ile Gly Leu Val Met Gly Tyr Asn His Phe Phe His Pro Asp Lys  
 50 55 60  
 Ile Leu Gly Leu Arg Tyr Phe Ala Phe Leu Asp Trp Gln Gly Tyr Gly  
 65 70 75 80  
 Met Arg Tyr Pro Lys Gly Tyr Tyr Gly Gly Asn Asn Met Ile Thr Tyr  
 85 90 95  
 Gly Val Gly Val Asp Ala Val Trp Asn Phe Phe Gln Gly Ser Phe Tyr  
 100 105 110  
 Gln Asp Asp Ile Ser Val Asp Ile Gly Val Phe Gly Gly Ile Ala Ile  
 115 120 125  
 Ala Gly Asn Ser Trp Tyr Ile Gly Ser Lys Gly Gln Glu Leu Leu Gly  
 130 135 140  
 Ile Thr Asn Ser Ser Ala Val Asp Asn Thr Ser Phe Gln Phe Leu Phe  
 145 150 155 160  
 Asn Phe Gly Leu Lys Ala Leu Phe Val Asp Glu His Glu Phe Glu Ile  
 165 170 175  
 Gly Phe Lys Phe Pro Thr Ile Asn Asn Lys Tyr Tyr Thr Thr Asp Ala  
 180 185 190  
 Leu Lys Val Gln Met Arg Arg Val Phe Ala Phe Tyr Val Gly Tyr Asn  
 195 200 205  
 Tyr His Phe  
 210

<210> 309  
 <211> 517  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(464)

<400> 309  
 agatttcatt cgaggtagaa aatacattga aaaagcgtgt gaattaaacg atg gta 56  
 Met Val  
 1  
 ggg ggt gga acg gta aaa aaa gac ttg aag aaa gcc att caa tac tat 104  
 Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr  
 5 10 15  
 gtt aaa gcg tgt gaa ttg aat gaa atg ttt ggg tgt ctg tca tta gtt 152  
 Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val  
 20 25 30  
 tcg aac tct caa ata aac aaa caa aaa ctc ttt caa tat ctc tct aaa 200  
 Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys

35	40	45	50												
gct tgt gaa tta aat agt ggt aat gga tgt agg ttt tta ggg gat ttt				248											
Ala Cys Glu Leu Asn Ser Gly Asn Gly Cys Arg Phe Leu Gly Asp Phe															
	55	60	65												
tat gag aat gga aaa tat gta aaa aag gat tta aga aaa gct gct caa				296											
Tyr Glu Asn Gly Lys Tyr Val Lys Lys Asp Leu Arg Lys Ala Ala Gln															
	70	75	80												
tac tac tct aaa gct tgt gga tta aat gat caa gat ggg tgt tta ata				344											
Tyr Tyr Ser Lys Ala Cys Gly Leu Asn Asp Gln Asp Gly Cys Leu Ile															
	85	90	95												
cta gga tat aag caa tat gct ggc aag ggc gta gtc aaa aat gaa aaa				392											
Leu Gly Tyr Lys Gln Tyr Ala Gly Lys Gly Val Val Lys Asn Glu Lys															
	100	105	110												
caa gcg gtg aaa acc ttt gaa aag gct tgt agg tta gga tct gaa gac				440											
Gln Ala Val Lys Thr Phe Glu Lys Ala Cys Arg Leu Gly Ser Glu Asp															
	115	120	125	130											
gca tgt ggt att tta aac aac tac tagatttgaa ataaatgctg ttttttagct				494											
Ala Cys Gly Ile Leu Asn Asn Tyr															
	135														
ggctttcatg tttttgtaac ccc				517											
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<213> Helicobacter pylori															
<400> 310															
Met	Val	Gly	Gly	Gly	Thr	Val	Lys	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Gln
1				5					10					15	
Tyr	Tyr	Val	Lys	Ala	Cys	Glu	Leu	Asn	Glu	Met	Phe	Gly	Cys	Leu	Ser
			20					25					30		
Leu	Val	Ser	Asn	Ser	Gln	Ile	Asn	Lys	Gln	Lys	Leu	Phe	Gln	Tyr	Leu
		35					40					45			
Ser	Lys	Ala	Cys	Glu	Leu	Asn	Ser	Gly	Asn	Gly	Cys	Arg	Phe	Leu	Gly
	50					55					60				
Asp	Phe	Tyr	Glu	Asn	Gly	Lys	Tyr	Val	Lys	Lys	Asp	Leu	Arg	Lys	Ala
	65				70					75				80	
Ala	Gln	Tyr	Tyr	Ser	Lys	Ala	Cys	Gly	Leu	Asn	Asp	Gln	Asp	Gly	Cys
				85					90					95	
Leu	Ile	Leu	Gly	Tyr	Lys	Gln	Tyr	Ala	Gly	Lys	Gly	Val	Val	Lys	Asn
			100					105					110		
Glu	Lys	Gln	Ala	Val	Lys	Thr	Phe	Glu	Lys	Ala	Cys	Arg	Leu	Gly	Ser
		115					120					125			
Glu	Asp	Ala	Cys	Gly	Ile	Leu	Asn	Asn	Tyr						
	130					135									
<210> 311															
<211> 451															
<212> DNA															
<213> Helicobacter pylori															
<220>															

[illegible]

gtggaacgct ctgtcttagc aaattgatct tagcggcgtc gtttttgata gtg gat 56  
Val Asp  
1

tca gag ggg ttt tcg cct tct att tat acc gac aag aca ggg cat ccc 104  
Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly His Pro  
5 10 15

acg att ggc tat ggc tat aat ttg agc gtt tat tct tat gag ggt aag 152  
Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu Gly Lys  
20 25 30

cgt atc acc aaa aca tat ggg ctt tta act gac ata ctc tct tat ggg 200  
Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser Tyr Gly  
35 40 45 50

ttg	tat	aaa	aat	ttg	gac	gca	atg	agg	aga	atg	gtc	atc	ttg	gat	ttg	248
Trp	Tyr	Lys	Asn	Leu	Asp	Ala	Met	Arg	Arg	Met	Val	Ile	Leu	Asp	Leu	
				55					60					65		

agc tac aat tta ggc ttg aac gga ctg ctc aaa ttc aag caa ttc atc      296  
Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln Phe Ile  
70 75 80

aag gcc ata gag gat aaa aat tat gct ttg gct gtg gag aga ctg caa 344  
Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg Leu Gln  
85 90 95

aaa agc ccg tat ttc aat caa gtg aaa aaa gag cgt caa gga ata tgg 392  
Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly Ile Trp  
100 105 110

aaa ttt tgaaattgga gggttgcgaa aaacattgta agaaaaaata cgcaatagaa 448  
Lys Phe  
115

aag 451

<210> 312

<211> 116

<212> PRT

<213> Helicobacter pylori

 $\langle 400 \rangle$  312

Val 1	Asp	Ser	Glu	Gly 5	Phe	Ser	Pro	Ser	Ile 10	Tyr	Thr	Asp	Lys	Thr 15	Gly
His	Pro	Thr	Ile	Gly 20	Tyr	Gly	Tyr	Asn 25	Leu	Ser	Val	Tyr	Ser 30	Tyr	Glu
Gly	Lys	Arg	Ile	Thr 35	Lys	Thr	Tyr 40	Gly	Leu	Leu	Thr	Asp 45	Ile	Leu	Ser
Tyr	Gly 50	Trp	Tyr	Lys	Asn 55	Leu	Asp	Ala	Met	Arg	Arg 60	Met	Val	Ile	Leu
Asp 65	Leu	Ser	Tyr	Asn 70	Leu	Gly	Leu	Asn	Gly	Leu 75	Leu	Lys	Phe	Lys 80	Gln
Phe	Ile	Lys	Ala	Ile	Glu	Asp	Lys	Asn	Tyr	Ala	Leu	Ala	Val	Glu	Arg





[illegible]

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<220>
<221> CDS
<222> (51)...(470)
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-363-

<210> 316  
 <211> 140  
 <212> PRT  
 <213> Helicobacter pylori

<400> 316  
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 1 5 10 15  
 Val Leu Leu Gly Leu Trp Arg Leu Thr Tyr Asp Lys Phe Tyr Phe Ser  
 20 25 30  
 Leu Val Phe Val Leu Leu Ile Leu Gly Ile Val Ala Cys Ser Tyr Ile  
 35 40 45  
 Ser Leu Lys Met His Gln Arg Lys Cys Phe Ala Lys Cys Phe Val Asn  
 50 55 60  
 Ser Glu Ser Phe Leu Ser Lys Met Leu His Ser Pro Ile Met Val Ile  
 65 70 75 80  
 Cys Phe Tyr Phe Ile Phe Ser Ile Phe Thr Ser Ile Ser Ile Val Tyr  
 85 90 95  
 Ser Val Leu Asp Tyr Asp Gln Met Met Trp Gly Phe Val Phe Cys Thr  
 100 105 110  
 Ile Val Val Cys Ala Val Val Phe Gly Thr Leu Glu Lys Asn Ala Gln  
 115 120 125  
 Glu Tyr His Gln Arg Arg Leu Phe Asp Ala Asp Val  
 130 135 140

<210> 317  
 <211> 976  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(923)

<400> 317  
 cccactgaag cgtattctaa caccctttta gaattagcta aaaaagatga aaa aat 56  
 Lys Asn  
 1  
 cgt agg cgt aac cgc ggc gat gct agc ggc aca gga tta gac aaa ctc 104  
 Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp Lys Leu  
 5 10 15  
 att gac gct tan cct ttg cgc ttt ttt gat gtc gct atc gct gag caa 152  
 Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala Glu Gln  
 20 25 30  
 cac gct tta act tct agc agc gct atg gct aaa gag ggg ttt aaa cct 200  
 His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe Lys Pro  
 35 40 45 50  
 ttt gtg agc atc tat tct act ttt ttg cag agg gct tat gat tct att 248  
 Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Ser Ile  
 55 60 65  
 gtg cat gac gct tgt att tct agc ttg ccg att aaa tta gcc att gac 296  
 Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala Ile Asp  
 70 75 80

agg gct ggg att gtg ggc gaa gat ggc gag acg cac caa ggg ctt tta	344
Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly Leu Leu	
85 90 95	
gac gtg tcg tat ttg cgc tct atc cct aac atg gtc att ttt gcc cca	392
Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe Ala Pro	
100 105 110	
cga gac aat gag act tta aaa aac gcc gtg cgt ttt gcc aat gaa cac	440
Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn Glu His	
115 120 125 130	
gat tca agc cct tgc gcg ttc cga tac cct agg ggg tcg ttt gcg tta	488
Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe Ala Leu	
135 140 145	
aaa gag ggg gtt ttt gag cct agc ggt ttt gtt tta ggc caa agc gaa	536
Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln Ser Glu	
150 155 160	
ttg ttg aaa aaa gag ggc gaa att tta ctc ata ggc tat ggt aat ggc	584
Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly Asn Gly	
165 170 175	
gtg ggg cgg gcg cat tta gtc caa ctg gct tta aaa gaa aaa aac ata	632
Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys Asn Ile	
180 185 190	
gaa tgc gct ctc ttg gat ctc agg ttt tta aag cct tta gat cca aat	680
Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp Pro Asn	
195 200 205 210	
tta agc gcg atc gtt gcc cct tat caa aag ctc tat gtt ttt agc gat	728
Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe Ser Asp	
215 220 225	
aat tac aag ctt gga ggg gtg gct agc gcg att tta gag ttt ttg agc	776
Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe Leu Ser	
230 235 240	
gaa caa aat att tta aag cct gtt aaa agc ttt gaa atc att gat gaa	824
Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile Asp Glu	
245 250 255	
ttt atc atg cat ggg aac acc gct tta gtg gaa aaa tcc tta gga tta	872
Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu Gly Leu	
260 265 270	
gac aca gag agt ttg act gac gct att tta aaa gat tta gga caa gag	920
Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly Gln Glu	
275 280 285 290	
aga tgaaaacaaa agcgccaatg aaaaatatcc gcaatttttc cattatcgct	973
cac	976

<210> 318

<211> 291

<212> PRT

<213> Helicobacter pylori

<400> 318  
 Lys Asn Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp  
 1 5 10 15  
 Lys Leu Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala  
 20 25 30  
 Glu Gln His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe  
 35 40 45  
 Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp  
 50 55 60  
 Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala  
 65 70 75 80  
 Ile Asp Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly  
 85 90 95  
 Leu Leu Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe  
 100 105 110  
 Ala Pro Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn  
 115 120 125  
 Glu His Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe  
 130 135 140  
 Ala Leu Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln  
 145 150 155 160  
 Ser Glu Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly  
 165 170 175  
 Asn Gly Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys  
 180 185 190  
 Asn Ile Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp  
 195 200 205  
 Pro Asn Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe  
 210 215 220  
 Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe  
 225 230 235 240  
 Leu Ser Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile  
 245 250 255  
 Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu  
 260 265 270  
 Gly Leu Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly  
 275 280 285  
 Gln Glu Arg  
 290

<210> 319  
 <211> 1135  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1082)

<400> 319  
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 Met Ala  
 1  
 tta tta ttc aca gga gcg tgc ggg tat ata ggc tcg cat acc gca agg 104  
 Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr Ala Arg  
 5 10 15  
 gcg ttt tta gaa aaa acc aaa gaa aat atc att att gta gat gac tta 152



gaa aaa aat aag agc gag atc tat aat gtc ggc tac aat caa ggc cat	872
Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln Gly His	
260 265 270	
agc gtg aaa gaa gtg ata gaa aag gtc aaa gaa atc tca aac aac gat	920
Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn Asn Asp	
275 280 285 290	
ttt tta gtg gaa att tta gac aaa cga cag ggc gat cca gca agc ctt	968
Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala Ser Leu	
295 300 305	
att gcc aat aac gct aaa atc tta caa aac acc tct ttc aaa ccc ctt	1016
Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys Pro Leu	
310 315 320	
tat aac aac cta gac acc att atc aaa agc gct cta gat tgg gaa gaa	1064
Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp Glu Glu	
325 330 335	
cac ctt ttg agg ttt caa taatacaccc tgtgcaaata caagccatta	1112
His Leu Leu Arg Phe Gln	
340	
gccattatgg gcgttcttat agt	1135
<210> 320	
<211> 344	
<212> PRT	
<213> Helicobacter pylori	
<400> 320	
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1 5 10 15	
Ala Arg Ala Phe Leu Glu Lys Thr Lys Glu Asn Ile Ile Ile Val Asp	
20 25 30	
Asp Leu Ser Thr Gly Phe Leu Glu His Leu Lys Ala Leu Glu His Tyr	
35 40 45	
Tyr Pro Asn Arg Val Val Phe Ile Gln Ala Asn Leu Asn Glu Thr His	
50 55 60	
Lys Leu Asp Ala Phe Leu Asn Lys Gln Gln Leu Lys Asp Pro Ile Glu	
65 70 75 80	
Ala Ile Leu His Phe Gly Ala Lys Ile Ser Val Glu Glu Ser Thr His	
85 90 95	
Leu Pro Leu Glu Tyr Tyr Thr Asn Asn Thr Leu Asn Thr Leu Glu Leu	
100 105 110	
Val Lys Leu Cys Leu Lys His Ala Ile Lys Arg Phe Ile Phe Ser Ser	
115 120 125	
Thr Ala Val Val Tyr Gly Glu Ser Ser Ser Ser Leu Asn Glu Glu Ser	
130 135 140	
Pro Leu Asn Pro Ile Asn Pro Tyr Gly Ala Ser Lys Met Met Ser Glu	
145 150 155 160	
Arg Ile Leu Leu Asp Thr Ser Lys Ile Ala Asp Phe Lys Cys Val Ile	
165 170 175	
Leu Arg Tyr Phe Asn Val Ala Gly Ala Cys Met His Asn Asp Tyr Thr	
180 185 190	
Thr Pro Tyr Thr Leu Gly Gln Arg Thr Leu Asn Ala Thr His Leu Ile	
195 200 205	
Lys Ile Ala Cys Glu Cys Ala Val Gly Lys Arg Lys Lys Met Gly Ile	







<210> 322  
 <211> 341  
 <212> PRT  
 <213> Helicobacter pylori

<400> 322

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1				5					10					15	
Val	Asn	Glu	Arg	Lys	Ile	Phe	Gly	Gly	Asn	Pro	Thr	Ser	Met	Phe	Asp
			20					25					30		
Leu	Asn	Lys	Ile	Lys	Tyr	Gln	Trp	Ala	Asp	His	Leu	Trp	Lys	Thr	Met
		35					40					45			
Leu	Ala	Asn	Thr	Trp	Phe	Ala	Glu	Glu	Val	Ser	Met	Asn	Asp	Asp	Lys
		50				55					60				
Arg	Asp	Tyr	Leu	Lys	Leu	Ser	Ala	Glu	Glu	Lys	Ile	Gly	Tyr	Asp	Arg
65					70					75					80
Ala	Leu	Ala	Gln	Leu	Ile	Phe	Met	Asp	Ser	Leu	Gln	Ala	Asn	Asn	Leu
				85					90					95	
Ile	Asp	Asn	Ile	Asn	Pro	Phe	Ile	Thr	Ser	Pro	Glu	Ile	Asn	Leu	Cys
			100					105						110	
Leu	Val	Arg	Gln	Ala	Tyr	Glu	Glu	Ala	Leu	His	Ser	His	Ala	Tyr	Ala
			115					120					125		
Val	Met	Val	Glu	Ser	Ile	Ser	Ala	Asn	Thr	Glu	Glu	Ile	Tyr	Asp	Met
			130				135					140			
Trp	Arg	Asn	Asp	Met	Gln	Leu	Lys	Ser	Lys	Asn	Asp	Tyr	Ile	Ala	Gln
145					150					155					160
Val	Tyr	Met	Glu	Leu	Ala	Lys	Asn	Pro	Thr	Glu	Glu	Asn	Ile	Leu	Lys
				165					170					175	
Ala	Leu	Phe	Ala	Asn	Gln	Ile	Leu	Glu	Gly	Ile	Tyr	Phe	Tyr	Ser	Gly
			180					185					190		
Phe	Ser	Tyr	Phe	Tyr	Thr	Leu	Ala	Arg	Ser	Gly	Lys	Met	Leu	Gly	Ser
		195					200					205			
Ala	Gln	Met	Ile	Arg	Phe	Ile	Gln	Arg	Asp	Glu	Val	Thr	His	Leu	Ile
		210				215					220				
Leu	Phe	Gln	Asn	Met	Ile	Asn	Ala	Leu	Arg	Asn	Glu	Arg	Ala	Asp	Leu
225					230					235					240
Phe	Thr	Pro	Gln	Leu	Ile	Asn	Glu	Val	Ile	Gly	Met	Phe	Lys	Lys	Ala
				245						250				255	
Val	Glu	Ile	Glu	Ala	Leu	Trp	Gly	Asp	Tyr	Ile	Thr	Gln	Gly	Lys	Ile
			260					265					270		
Leu	Gly	Leu	Thr	Ser	Ser	Leu	Ile	Glu	Gln	Tyr	Ile	Gln	Phe	Leu	Ala
			275				280					285			
Asp	Ser	Arg	Leu	Ser	Lys	Val	Gly	Ile	Ala	Lys	Val	Tyr	Gly	Val	Gln
		290				295					300				
His	Pro	Ile	Lys	Trp	Val	Glu	Ser	Phe	Ser	Ser	Phe	Asn	Glu	Gln	Arg
305					310					315					320
Ser	Asn	Phe	Phe	Glu	Ala	Arg	Val	Ser	Asn	Tyr	Ala	Lys	Gly	Ser	Val
				325					330					335	
Ser	Phe	Asp	Asp	Phe											
			340												

<210> 323  
 <211> 689  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (139)...(627)



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 Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr Ala Glu Asp Pro Lys  
 50 55 60  
 Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu Trp Ile Ala Pro Gly  
 65 70 75 80  
 Gly Val Asn Val Arg Leu Asp Ser His Ala His Ala Asn Tyr Val Val  
 85 90 95  
 Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu Ile Val Trp Gly Glu  
 100 105 110  
 Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg Ala Leu Lys Glu Phe  
 115 120 125  
 Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe His Leu Glu Met Leu  
 130 135 140  
 Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His Thr Lys Tyr Leu Glu  
 145 150 155 160  
 Glu Asn Phe

<210> 325  
 <211> 1960  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1907)

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 Met Phe  
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 Tyr His Leu Ile Ala Pro Leu Lys Asn Lys Thr Pro Pro Leu Thr Tyr  
 5 10 15  
 ttt tct aaa gag caa cac caa aaa gga gcg tta gtc aat atc cct tta 152  
 Phe Ser Lys Glu Gln His Gln Lys Gly Ala Leu Val Asn Ile Pro Leu  
 20 25 30  
 agg aat aaa acg ctt tta ggc gtc gtc ctt gaa gaa gtt tca aaa ccc 200  
 Arg Asn Lys Thr Leu Leu Gly Val Val Leu Glu Glu Val Ser Lys Pro  
 35 40 45 50  
 tct ttt gaa tgc cta gag cta gaa aaa acc cct tat ttt tta ctc ccc 248  
 Ser Phe Glu Cys Leu Glu Leu Glu Lys Thr Pro Tyr Phe Leu Leu Pro  
 55 60 65  
 ttt caa atg gag ctc gct att ttt atc gct caa tat tac tca gct aat 296  
 Phe Gln Met Glu Leu Ala Ile Phe Ile Ala Gln Tyr Tyr Ser Ala Asn  
 70 75 80  
 ctt tct tca gtt tta agc ctt ttt gcc cct ttt aaa gaa tgc gat tta 344  
 Leu Ser Ser Val Leu Ser Leu Phe Ala Pro Phe Lys Glu Cys Asp Leu  
 85 90 95  
 gtg ggg tta gaa aaa att gag cct att ctt aat ata tta agc caa acg 392  
 Val Gly Leu Glu Lys Ile Glu Pro Ile Leu Asn Ile Leu Ser Gln Thr





tat cgc tac ctt att tta ttg cgt tcc aaa aac cct tta agc cta atc 1832  
 Tyr Arg Tyr Leu Ile Leu Leu Arg Ser Lys Asn Pro Leu Ser Leu Ile  
 580 585 590

aaa agc gtg cat gcg ttt tta aaa tcc gcc cct agt atc cct tgc agc 1880  
 Lys Ser Val His Ala Phe Leu Lys Ser Ala Pro Ser Ile Pro Cys Ser  
 595 600 605 610

gtg aac atg gat cct gtg gat att ttt taaaaaactc atgttttata 1927  
 Val Asn Met Asp Pro Val Asp Ile Phe  
 615

tattatttca aaaaacttaa gtttttctgg cga 1960

<210> 326  
 <211> 619  
 <212> PRT  
 <213> Helicobacter pylori

<400> 326  
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 20 25 30  
 Pro Leu Arg Asn Lys Thr Leu Leu Gly Val Val Leu Glu Glu Val Ser  
 35 40 45  
 Lys Pro Ser Phe Glu Cys Leu Glu Leu Glu Lys Thr Pro Tyr Phe Leu  
 50 55 60  
 Leu Pro Phe Gln Met Glu Leu Ala Ile Phe Ile Ala Gln Tyr Tyr Ser  
 65 70 75 80  
 Ala Asn Leu Ser Ser Val Leu Ser Leu Phe Ala Pro Phe Lys Glu Cys  
 85 90 95  
 Asp Leu Val Gly Leu Glu Lys Ile Glu Pro Ile Leu Asn Ile Leu Ser  
 100 105 110  
 Gln Thr Gln Thr Asn Ala Leu Lys Glu Leu Gln Lys His Ser Ala Ser  
 115 120 125  
 Leu Leu Phe Gly Asp Thr Gly Ser Gly Lys Thr Glu Ile Tyr Met His  
 130 135 140  
 Ala Ile Ala Gln Thr Leu Glu Gln Lys Lys Ser Ala Leu Leu Leu Val  
 145 150 155 160  
 Pro Glu Ile Ala Leu Thr Pro Gln Met Gln Gln Arg Leu Lys Arg Val  
 165 170 175  
 Phe Lys Glu Asn Leu Gly Leu Trp His Ser Lys Leu Ser Gln Asn Gln  
 180 185 190  
 Lys Lys Gln Phe Leu Glu Lys Leu Tyr Ser Gln Glu Ile Lys Leu Val  
 195 200 205  
 Val Gly Thr Arg Ser Ala Leu Phe Leu Pro Leu Lys Glu Leu Gly Leu  
 210 215 220  
 Ile Ile Val Asp Glu Glu His Asp Phe Ser Tyr Lys Ser His Gln Ser  
 225 230 235 240  
 Pro Met Tyr Asn Ala Arg Asp Leu Cys Leu Tyr Leu Ser His Lys Phe  
 245 250 255  
 Pro Ile Gln Val Ile Leu Gly Ser Ala Thr Pro Ser Leu Asn Ser Tyr  
 260 265 270  
 Lys Arg Phe Lys Asp Lys Ala Leu Val Arg Leu Lys Gly Arg Tyr Thr  
 275 280 285  
 Pro Thr Gln Lys Asn Ile Ile Phe Glu Lys Thr Glu Arg Phe Ile Thr  
 290 295 300  
 Pro Lys Leu Leu Glu Ala Leu Gln Gln Val Leu Asp Lys Asn Glu Gln







aca acc cct atg gat ttg agc gtg aaa aac gat gaa aac aac ctt gaa Thr Thr Pro Met Asp Leu Ser Val Lys Asn Asp Glu Asn Asn Leu Glu 270 275 280	927
agc gtt tat atc aac cat caa aaa cgc tcc acg atc gct atc aag cat Ser Val Tyr Ile Asn His Gln Lys Arg Ser Thr Ile Ala Ile Lys His 285 290 295	975
caa gtt caa aaa gat ttg agc gag tgt ttg ctt tta gag gca agt tac Gln Val Gln Lys Asp Leu Ser Glu Cys Leu Leu Leu Glu Ala Ser Tyr 300 305 310	1023
acc gat ccg ata agc ctg tct tta aaa tta cac gcc cta aaa gat aaa Thr Asp Pro Ile Ser Leu Ser Leu Lys Leu His Ala Leu Lys Asp Lys 315 320 325 330	1071
acg ctt caa aaa gac aac gcc ctt att tat aga agc gct agg ggg agt Thr Leu Gln Lys Asp Asn Ala Leu Ile Tyr Arg Ser Ala Arg Gly Ser 335 340 345	1119
aac cct aat tta tca gac ggc ttg aat ttt tta agc gct cat ttg aaa Asn Pro Asn Leu Ser Asp Gly Leu Asn Phe Leu Ser Ala His Leu Lys 350 355 360	1167
gcc acg att tta gaa agc aaa caa act gag cat tct tta aaa gat cgc Ala Thr Ile Leu Glu Ser Lys Gln Thr Glu His Ser Leu Lys Asp Arg 365 370 375	1215
acc ctt aca ttc cag ctt gaa gac att act gaa att ttg ggg ctt gct Thr Leu Thr Phe Gln Leu Glu Asp Ile Thr Glu Ile Leu Gly Leu Ala 380 385 390	1263
gta gag aaa gaa aaa att caa ggc att tta aaa aat tta ggc ttt aaa Val Glu Lys Glu Lys Ile Gln Gly Ile Leu Lys Asn Leu Gly Phe Lys 395 400 405 410	1311
gtc agc gta aaa gag cca aac tca aaa ccc caa att tta gag gtt att Val Ser Val Lys Glu Pro Asn Ser Lys Pro Gln Ile Leu Glu Val Ile 415 420 425	1359
gcg cca aat ttc agg cat gac att aaa acg atc caa gat att gct gaa Ala Pro Asn Phe Arg His Asp Ile Lys Thr Ile Gln Asp Ile Ala Glu 430 435 440	1407
gaa att ttg cgc ttt gta ggg att gat aat cta gtc tca aag ccc ctt Glu Ile Leu Arg Phe Val Gly Ile Asp Asn Leu Val Ser Lys Pro Leu 445 450 455	1455
cat tgt gtc agt agc aaa aat tca aac ccc aat tac gac acg cac cgc His Cys Val Ser Ser Lys Asn Ser Asn Pro Asn Tyr Asp Thr His Arg 460 465 470	1503
ttt ttt gaa aac ctt aaa cac aag gct ctc gct tgc ggt ttt aaa gaa Phe Phe Glu Asn Leu Lys His Lys Ala Leu Ala Cys Gly Phe Lys Glu 475 480 485 490	1551
gtc att cat tac gtg ttt tac tct aaa gaa aaa cag caa aaa tta ggc Val Ile His Tyr Val Phe Tyr Ser Lys Glu Lys Gln Gln Lys Leu Gly	1599

495	500	505	
ttt gaa gtt tta gaa gat ccc cta gaa ttg caa aac cct atc aca acg Phe Glu Val Leu Glu Asp Pro Leu Glu Leu Gln Asn Pro Ile Thr Thr 510 515 520			1647
gag tta aac acc cta agg acg agt ctt gtt tgc ggg ctt tta gac gcc Glu Leu Asn Thr Leu Arg Thr Ser Leu Val Cys Gly Leu Leu Asp Ala 525 530 535			1695
agt tta agg aat aaa aat tta ggg ttt aaa agc ata gcc ctt tat gaa Ser Leu Arg Asn Lys Asn Leu Gly Phe Lys Ser Ile Ala Leu Tyr Glu 540 545 550			1743
aag ggg agc gtg tat aac tct aaa aga gaa gaa atc caa aaa cta ggc Lys Gly Ser Val Tyr Asn Ser Lys Arg Glu Glu Ile Gln Lys Leu Gly 555 560 565 570			1791
ttt tta ata agc ggc ttg caa aaa aaa gaa agc tac cct gat act aag Phe Leu Ile Ser Gly Leu Gln Lys Lys Glu Ser Tyr Pro Asp Thr Lys 575 580 585			1839
ggc aag gct tgg gat ttt tac tct ttt gcc gaa tgc gtt tca aaa gtt Gly Lys Ala Trp Asp Phe Tyr Ser Phe Ala Glu Cys Val Ser Lys Val 590 595 600			1887
ata ggg gat ttc agc ttg gaa aaa cta acc act caa acc ccc att aac Ile Gly Asp Phe Ser Leu Glu Lys Leu Thr Thr Gln Thr Pro Ile Asn 605 610 615			1935
cac ccc tac cag agc gct aaa atc att caa aat cat gaa atc ata ggc His Pro Tyr Gln Ser Ala Lys Ile Ile Gln Asn His Glu Ile Ile Gly 620 625 630			1983
gtg atc gct aaa atc cac cct aaa gtg atc cag gaa ttg gat ttg ttt Val Ile Ala Lys Ile His Pro Lys Val Ile Gln Glu Leu Asp Leu Phe 635 640 645 650			2031
gaa agc tat tac gct gag ata gac gct ttt aaa ctc aaa cgc cct gct Glu Ser Tyr Tyr Ala Glu Ile Asp Ala Phe Lys Leu Lys Arg Pro Ala 655 660 665			2079
atg cta tta aaa ccc ttt agc att tat cct agc agt gtt agg gat ttg Met Leu Leu Lys Pro Phe Ser Ile Tyr Pro Ser Ser Val Arg Asp Leu 670 675 680			2127
act ctc atc att gat gag aat acc gct ttt agt ggg att aaa aaa gcc Thr Leu Ile Ile Asp Glu Asn Thr Ala Phe Ser Gly Ile Lys Lys Ala 685 690 695			2175
cta aag gac gct caa atc cct aat tta agc gag att cta ccc ctt gat Leu Lys Asp Ala Gln Ile Pro Asn Leu Ser Glu Ile Leu Pro Leu Asp 700 705 710			2223
att ttt aaa gaa agt aat aat tcc ata gcc tta agc gtg cgt tgc gtg Ile Phe Lys Glu Ser Asn Asn Ser Ile Ala Leu Ser Val Arg Cys Val 715 720 725 730			2271
atc cat tct tta gaa aaa acc ctg aat gat gaa gag gtc aat tca gcc			2319



Ser Leu Lys Leu His Ala Leu Lys Asp Lys Thr Leu Gln Lys Asp Asn  
325 330 335  
Ala Leu Ile Tyr Arg Ser Ala Arg Gly Ser Asn Pro Asn Leu Ser Asp  
340 345 350  
Gly Leu Asn Phe Leu Ser Ala His Leu Lys Ala Thr Ile Leu Glu Ser  
355 360 365  
Lys Gln Thr Glu His Ser Leu Lys Asp Arg Thr Leu Thr Phe Gln Leu  
370 375 380  
Glu Asp Ile Thr Glu Ile Leu Gly Leu Ala Val Glu Lys Glu Lys Ile  
385 390 395 400  
Gln Gly Ile Leu Lys Asn Leu Gly Phe Lys Val Ser Val Lys Glu Pro  
405 410 415  
Asn Ser Lys Pro Gln Ile Leu Glu Val Ile Ala Pro Asn Phe Arg His  
420 425 430  
Asp Ile Lys Thr Ile Gln Asp Ile Ala Glu Glu Ile Leu Arg Phe Val  
435 440 445  
Gly Ile Asp Asn Leu Val Ser Lys Pro Leu His Cys Val Ser Ser Lys  
450 455 460  
Asn Ser Asn Pro Asn Tyr Asp Thr His Arg Phe Glu Asn Leu Lys  
465 470 475 480  
His Lys Ala Leu Ala Cys Gly Phe Lys Glu Val Ile His Tyr Val Phe  
485 490 495  
Tyr Ser Lys Glu Lys Gln Gln Lys Leu Gly Phe Glu Val Leu Glu Asp  
500 505 510  
Pro Leu Glu Leu Gln Asn Pro Ile Thr Thr Glu Leu Asn Thr Leu Arg  
515 520 525  
Thr Ser Leu Val Cys Gly Leu Leu Asp Ala Ser Leu Arg Asn Lys Asn  
530 535 540  
Leu Gly Phe Lys Ser Ile Ala Leu Tyr Glu Lys Gly Ser Val Tyr Asn  
545 550 555 560  
Ser Lys Arg Glu Glu Ile Gln Lys Leu Gly Phe Leu Ile Ser Gly Leu  
565 570 575  
Gln Lys Lys Glu Ser Tyr Pro Asp Thr Lys Gly Lys Ala Trp Asp Phe  
580 585 590  
Tyr Ser Phe Ala Glu Cys Val Ser Lys Val Ile Gly Asp Phe Ser Leu  
595 600 605  
Glu Lys Leu Thr Thr Gln Thr Pro Ile Asn His Pro Tyr Gln Ser Ala  
610 615 620  
Lys Ile Ile Gln Asn His Glu Ile Ile Gly Val Ile Ala Lys Ile His  
625 630 635 640  
Pro Lys Val Ile Gln Glu Leu Asp Leu Phe Glu Ser Tyr Tyr Ala Glu  
645 650 655  
Ile Asp Ala Phe Lys Leu Lys Arg Pro Ala Met Leu Leu Lys Pro Phe  
660 665 670  
Ser Ile Tyr Pro Ser Ser Val Arg Asp Leu Thr Leu Ile Ile Asp Glu  
675 680 685  
Asn Thr Ala Phe Ser Gly Ile Lys Lys Ala Leu Lys Asp Ala Gln Ile  
690 695 700  
Pro Asn Leu Ser Glu Ile Leu Pro Leu Asp Ile Phe Lys Glu Ser Asn  
705 710 715 720  
Asn Ser Ile Ala Leu Ser Val Arg Cys Val Ile His Ser Leu Glu Lys  
725 730 735  
Thr Leu Asn Asp Glu Glu Val Asn Ser Ala Val Gln Lys Ala Leu Glu  
740 745 750  
Ile Leu Glu Lys Glu Phe Asn Ala Arg Leu Lys Gly  
755 760

<210> 329

<211> 1097

<212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (492)...(1040)

<400> 329

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tgaatgcttt	gggtaaaaaa	ggggtttttg	cggataaatt	caaccagctc	aaacatctga	180
acggcgaaga	aaaaaacgcc	tttgctaaag	aatccacca	ttataaacia	gcgtttgaaa	240
aagcctttga	atggaaaaaa	aaggctatta	tagagcttga	attagaagaa	cgcttgaaaa	300
aagaaaaaat	tgatgtgagc	ttgtttaacg	ctatcaaaac	aagctcttct	caccctttaa	360
actacactaa	aaataaaatc	attgaatttt	tcaccccat	aggatacaag	cttgaaatcg	420
gctctttagt	ggaagatgat	ttccataatt	tcagcgttt	aaacttgccc	ccttaccatc	480
ctgcaagaga	c atg caa gac act ttt tat ttt aaa gat cac aag ctt tta					530
	Met Gln Asp Thr Phe Tyr Phe Lys Asp His Lys Leu Leu					
	1 5 10					
agg acc cac act tcg ccc gtg caa atc cac acc atg caa gaa caa acc						578
Arg Thr His Thr Ser Pro Val Gln Ile His Thr Met Gln Glu Gln Thr						
15 20 25						
cca ccc att aag atg att tgt tta ggc gaa acc ttt agg cgc gat tat						626
Pro Pro Ile Lys Met Ile Cys Leu Gly Glu Thr Phe Arg Arg Asp Tyr						
30 35 40 45						
gat ttg acc cac acg ccc atg ttc cac caa att gaa ggg ctt gtc gtg						674
Asp Leu Thr His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val						
50 55 60						
gat caa aaa ggg aat atc cgt ttc aca cat tta aaa ggt gtg atc gaa						722
Asp Gln Lys Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu						
65 70 75						
gac ttt ttg cat tat ttc ttt ggg ggc gtg aag tta agg tgg cgc tct						770
Asp Phe Leu His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser						
80 85 90						
agc ttt ttc cct ttc aca gag cca agc gct gaa gtg gat att agt tgc						818
Ser Phe Phe Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys						
95 100 105						
gtg ttt tgc aag caa gaa ggc tgt agg gtt tgc tcg cac aca ggc tgg						866
Val Phe Cys Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp						
110 115 120 125						
tta gaa gtg ttg ggc tgt ggc atg gtc aat aat gcg gtg ttt gaa gcc						914
Leu Glu Val Leu Gly Cys Gly Met Val Asn Asn Ala Val Phe Glu Ala						
130 135 140						
ata ggg tat gag aat gtg agc ggg ttt gct ttt ggc atg ggg att gaa						962
Ile Gly Tyr Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu						
145 150 155						
aga tta gcc atg ctg act tgc cag atc aat gat ttg cgc agt ttc ttt						1010
Arg Leu Ala Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe						
160 165 170						

gaa act gat ttg aga gtg ttg gag agc ttt taatgaaact gagcattaat 1060  
 Glu Thr Asp Leu Arg Val Leu Glu Ser Phe  
 175 180

gatttgaatg tttttgtcaa tacgcctaaa gatatag 1097

<210> 330  
 <211> 183  
 <212> PRT  
 <213> Helicobacter pylori

<400> 330  
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 Lys Met Ile Cys Leu Gly Glu Thr Phe Arg Arg Asp Tyr Asp Leu Thr  
 35 40 45  
 His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val Asp Gln Lys  
 50 55 60  
 Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu Asp Phe Leu  
 65 70 75 80  
 His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser Ser Phe Phe  
 85 90 95  
 Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys Val Phe Cys  
 100 105 110  
 Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp Leu Glu Val  
 115 120 125  
 Leu Gly Cys Gly Met Val Asn Asn Ala Val Phe Glu Ala Ile Gly Tyr  
 130 135 140  
 Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu Arg Leu Ala  
 145 150 155 160  
 Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe Glu Thr Asp  
 165 170 175  
 Leu Arg Val Leu Glu Ser Phe  
 180

<210> 331  
 <211> 517  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(464)

<400> 331  
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 Met Lys  
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aaa att gat gat atg aga cac gga aga cat tgt gtt ttt tta atg cat 104  
 Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His  
 5 10 15

gtg cat ttt gta ttt gtt act aaa tac agg cgt tca gca ttc aat aag 152  
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 20 25 30



<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1733)

<400> 333

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gaa gtc cat gat tat ggg att aaa ttt tgg agc aat aac gaa ttt aag	104
Glu Val His Asp Tyr Gly Ile Lys Phe Trp Ser Asn Asn Glu Phe Lys	
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Ile Glu Lys Gly Leu Val Lys Val Cys His Gly Lys Asn Pro Ser Leu	
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tta gaa atc gtt caa agc gtg cgc gat aag ggc tat aga gga cct ttg	200
Leu Glu Ile Val Gln Ser Val Arg Asp Lys Gly Tyr Arg Gly Pro Leu	
35 40 45 50	
ttg gtg cga ttc ccc cat ttg gtg caa aaa caa atc aaa agc ctg ttt	248
Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser Leu Phe	
55 60 65	
gat gcg ttt tct tca gcg att aaa gag tat caa tac agc ggg gct ttt	296
Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly Ala Phe	
70 75 80	
aag gcg gtt ttc cct tta aaa gtc aat caa atg ccc tcg ttt gtt ttc	344
Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe Val Phe	
85 90 95	
cct tta gtg cag ggg gct aag ggt ttg aat tac gga tta gag gct ggg	392
Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu Ala Gly	
100 105 110	
agc aag tct gaa ctc atc atc gca atg agt tac act aac cct aaa gcc	440
Ser Lys Ser Glu Leu Ile Ile Ala Met Ser Tyr Thr Asn Pro Lys Ala	
115 120 125 130	
cct atc acc gtg aat ggc ttt aaa gac aaa gaa atg att gag ctt ggc	488
Pro Ile Thr Val Asn Gly Phe Lys Asp Lys Glu Met Ile Glu Leu Gly	
135 140 145	
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Phe Ile Ala Lys Ser Met Gln His Glu Ile Thr Leu Thr Ile Glu Gly	
150 155 160	
ttg aat gaa ttg aaa acc att atc gcc gtg gct aaa caa aac gag ttt	584
Leu Asn Glu Leu Lys Thr Ile Ile Ala Val Ala Lys Gln Asn Glu Phe	
165 170 175	
tta gcc tgc cct aaa att ggc atc cgc atc cgt ttg cac agc act ggc	632
Leu Ala Cys Pro Lys Ile Gly Ile Arg Ile Arg Leu His Ser Thr Gly	
180 185 190	



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agc Ser	agc Ser	act Thr	gaa Glu	gtt Val 215	tta Leu	gag Glu	gcg Ala	atg Met	cgc Arg 220	ctt Leu	tta Leu	gaa Glu	gaa Glu	aac Asn 225	gac Asp	728
ttg Leu	tta Leu	gag Glu	cat His 230	ttc Phe	cac His	atg Met	ata Ile	cat His	ttc Phe	cat His	ata Ile	ggc Gly	tct Ser 240	caa Gln	atc Ile	776
agc Ser	gat Asp	att Ile 245	tcg Ser	ccc Pro	tta Leu	aaa Lys	aag Lys 250	gct Ala	tta Leu	aga Arg	gaa Glu	gcg Ala 255	ggg Gly	aac Asn	ttg Leu	824
tat Tyr	gca Ala 260	gaa Glu	ttg Leu	cgt Arg	aaa Lys	atg Met 265	ggc Gly	gct Ala	aaa Lys	aat Asn	ctt Leu 270	aat Asn	agc Ser	gtg Val	aat Asn	872
att Ile 275	gga Gly	ggg Gly	ggg Gly	tta Leu	gcc Ala 280	gta Val	gaa Glu	tac Tyr	acc Thr	caa Gln 285	cac His	aag Lys	cac His	cac His	caa Gln 290	920
gac Asp	aaa Lys	aac Asn	tac Tyr	act Thr 295	tta Leu	gag Glu	gaa Glu	ttc Phe	agc Ser 300	gct Ala	gat Asp	gtg Val	gtg Val	ttt Phe 305	tta Leu	968
ttg Leu	aga Arg	gaa Glu	att Ile 310	gtg Val	aaa Lys	aat Asn	aag Lys	cag Gln 315	gaa Glu	atc Ile	gag Glu	ccg Pro	gac Asp 320	att Ile	ttc Phe	1016
att Ile	gaa Glu	tca Ser 325	ggc Gly	cgt Arg	tat Tyr	att Ile	tcc Ser 330	gct Ala	aac Asn	cat His	gcc Ala 335	gtt Val 335	tta Leu	gtg Val	gcc Ala	1064
ccg Pro	gtg Val 340	tta Leu	gaa Glu	ttg Leu	ttt Phe	tcg Ser 345	cat His	gaa Glu	tac Tyr	aat Asn	gaa Glu 350	aaa Lys	tcc Ser	cta Leu	aaa Lys	1112
atc Ile 355	aaa Lys	gaa Glu	aat Asn	aat Asn	aac Asn 360	ccc Pro	cct Pro	ttg Leu	att Ile	gat Asp 365	gaa Glu	atg Met	cta Leu	gac Asp	ttg Leu 370	1160
ctc Leu	gct Ala	aat Asn	atc Ile	aat Asn 375	gaa Glu	aaa Lys	aac Asn	gcc Ala	att Ile 380	gaa Glu	tac Tyr	ttg Leu	cat His	gat Asp 385	agt Ser	1208
ttt Phe	gat Asp	cac His	acc Thr 390	gag Glu	tcg Ser	cta Leu	ttc Phe	acg Thr 395	ctt Leu	ttt Phe	gat Asp	ctg Leu	ggc Gly 400	tat Tyr	att Ile	1256
gat Asp	ttg Leu	att Ile 405	gac Asp	agg Arg	agc Ser	aac Asn	act Thr 410	gaa Glu	gtt Val	tta Leu	gcc Ala 415	cat His 415	ttg Leu	atc Ile	gtc Val	1304
aaa Lys 420	aaa Lys	gcg Ala	gtg Val	caa Gln	ttg Leu	ctt Leu 425	tat Tyr	gtt Val	aag Lys	gat Asp	cat His 430	aac Asn	gat Asp	att Ile	tta Leu	1352

cgc att caa gag cag gtc caa gag cgc tat tta ttg aat tgc tcg ttt	1400
Arg Ile Gln Glu Gln Val Gln Glu Arg Tyr Leu Leu Asn Cys Ser Phe	
435 440 445 450	
ttc caa agc ttg ccg gat tat tgg ggc ttg aga cag aat ttc ccg gtc	1448
Phe Gln Ser Leu Pro Asp Tyr Trp Gly Leu Arg Gln Asn Phe Pro Val	
455 460 465	
atg ccc ttg aat aaa tta gat gaa aag ccc acc agg agt gcg agc ttg	1496
Met Pro Leu Asn Lys Leu Asp Glu Lys Pro Thr Arg Ser Ala Ser Leu	
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Trp Asp Ile Thr Cys Asp Ser Asp Gly Glu Ile Ala Phe Asp Ser Thr	
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Lys Pro Leu Phe Leu His Asp Ile Asp Ile Asp Glu Glu Glu Tyr Phe	
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Leu Ala Phe Phe Leu Val Gly Ala Tyr Gln Glu Val Leu Gly Met Lys	
515 520 525 530	
cac aat tta ttc acg cac cta cgg aat tta gcg tgg ttt ttg atg aaa	1688
His Asn Leu Phe Thr His Leu Arg Asn Leu Ala Trp Phe Leu Met Lys	
535 540 545	
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Lys Ala Ile Met Lys Trp Lys Ile Phe Val Lys Pro Lys Arg Phe	
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Ser Leu Leu Glu Ile Val Gln Ser Val Arg Asp Lys Gly Tyr Arg Gly	
35 40 45	
Pro Leu Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser	
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Leu Phe Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly	
65 70 75 80	
Ala Phe Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe	
85 90 95	
Val Phe Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu	
100 105 110	
Ala Gly Ser Lys Ser Glu Leu Ile Ile Ala Met Ser Tyr Thr Asn Pro	
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5 10 15	
tta acc aaa aga gtt aga aag aag att ttt aag aat gat ccc aca gaa	152
Leu Thr Lys Arg Val Arg Lys Lys Ile Phe Lys Asn Asp Pro Thr Glu	
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Asn Gln Lys Lys Ala Ile Lys Ile Ala Leu Asn Thr Pro Asp Ile Ala	
35 40 45 50	
att atc caa ggg cct cct gga acg ggc aaa acc act gtg atc aat gcc	248
Ile Ile Gln Gly Pro Pro Gly Thr Gly Lys Thr Thr Val Ile Asn Ala	
55 60 65	
att tgt gag aga ttg ttt gaa gaa tac cct aag gat aaa aat atc aag	296
Ile Cys Glu Arg Leu Phe Glu Glu Tyr Pro Lys Asp Lys Asn Ile Lys	
70 75 80	
ggg caa att tta ctg tgc gct caa ggg cat gat gcg act aac aat gcg	344
Gly Gln Ile Leu Leu Cys Ala Gln Gly His Asp Ala Thr Asn Asn Ala	
85 90 95	
cgt gag cgc atc aaa gta ggg gga ttg ccc act ttt aaa ttt ggt gct	392
Arg Glu Arg Ile Lys Val Gly Gly Leu Pro Thr Phe Lys Phe Gly Ala	
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Lys Lys Asn Ala Lys Glu Glu Gln Tyr Lys Gln Asp Glu Arg Leu Asn	
115 120 125 130	
gag cga ttg aga gag ttt gct gaa acg ctc ata gaa agc gtg aga aaa	488
Glu Arg Leu Arg Glu Phe Ala Glu Thr Leu Ile Glu Ser Val Arg Lys	
135 140 145	
aaa ctg caa aaa tta ggg gat tat gaa aat ata gaa aaa att ttg gat	536
Lys Leu Gln Lys Leu Gly Asp Tyr Glu Asn Ile Glu Lys Ile Leu Asp	
150 155 160	
tta gaa gaa gcc ctt aga cgc tac tat agt tcg cct atc agt gaa ttg	584
Leu Glu Glu Ala Leu Arg Arg Tyr Tyr Ser Ser Pro Ile Ser Glu Leu	
165 170 175	
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Glu Phe Leu Lys Glu Ile Glu Lys Asn Glu Ser Phe Phe	
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Thr	Glu	Asn	Gln	Lys	Lys	Ala	Ile	Lys	Ile	Ala	Leu	Asn	Thr	Pro	Asp
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Ile	Ala	Ile	Ile	Gln	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Thr	Val	Ile
	50					55					60				
Asn	Ala	Ile	Cys	Glu	Arg	Leu	Phe	Glu	Glu	Tyr	Pro	Lys	Asp	Lys	Asn
65					70					75					80
Ile	Lys	Gly	Gln	Ile	Leu	Leu	Cys	Ala	Gln	Gly	His	Asp	Ala	Thr	Asn
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Asn	Ala	Arg	Glu	Arg	Ile	Lys	Val	Gly	Gly	Leu	Pro	Thr	Phe	Lys	Phe
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Gly	Ala	Lys	Lys	Asn	Ala	Lys	Glu	Glu	Gln	Tyr	Lys	Gln	Asp	Glu	Arg
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Leu	Asn	Glu	Arg	Leu	Arg	Glu	Phe	Ala	Glu	Thr	Leu	Ile	Glu	Ser	Val
	130					135					140				
Arg	Lys	Lys	Leu	Gln	Lys	Leu	Gly	Asp	Tyr	Glu	Asn	Ile	Glu	Lys	Ile
145					150					155					160
Leu	Asp	Leu	Glu	Glu	Ala	Leu	Arg	Arg	Tyr	Tyr	Ser	Ser	Pro	Ile	Ser
				165					170					175	
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-391-



[illegible]

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Leu Glu Glu Leu Tyr Ala Pro Asn His Ile Glu Arg Leu Lys Ala Arg																	
5 10 15																	
agt ttt tta aga tcg att gct ttt ttt gat gat ttt agc gct tct ttt																	152
Ser Phe Leu Arg Ser Ile Ala Phe Phe Asp Asp Phe Ser Ala Ser Phe																	
20 25 30																	
gaa tac aga gat cta ttt agc gtt ttg gaa aat atc gtg caa ttt gat																	200
Glu Tyr Arg Asp Leu Phe Ser Val Leu Glu Asn Ile Val Gln Phe Asp																	

35	40										45					50					
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gtg Val	gag Glu	cca Pro	gcc Ala 70	cta Leu	aag Lys	gct Ala	atc Ile	ttt Phe 75	agc Ser	aat Asn	cta Leu	aat Asn	acc Thr 80	aat Asn	atc Ile	296					
tac Tyr	cga Arg	aaa Lys 85	cat His	tta Leu	aaa Lys	atg Met	cct Pro 90	tta Leu	gaa Glu	aag Lys	gct Ala	agg Arg 95	gaa Glu	ttt Phe	gac Asp	344					
gct Ala	aaa Lys 100	tgc Cys	gcg Ala	ttg Leu	gat Asp	tta Leu 105	gcc Ala	aag Lys	cga Arg	cca Pro	ggg Gly 110	cgt Arg	agt Ser	ttg Leu	aaa Lys	392					
gaa Glu 115	aag Lys	ttg Leu	tgc Cys	gac Asp	aat Asn 120	aaa Lys	gta Val	ttg Leu	agc Ser	gtc Val 125	aag Lys	cgt Arg	tat Tyr	gtg Val	aat Asn 130	440					
gcc Ala	aat Asn	acg Thr	cat His	gaa Glu 135	aac Asn	agg Arg	ttt Phe	ctc Leu	aag Lys 140	cgt Arg	ttc Phe	att Ile	aaa Lys	gaa Glu 145	ctt Leu	488					
tta Leu	aga Arg	ata Ile	att Ile 150	cat His	tgg Trp	cgc Arg	gag Glu	ata Ile 155	gaa Glu	ttc Phe	caa Gln	cag Gln	ggt Val 160	ttt Phe	gaa Glu	536					
gag Glu	tta Leu 165	att Ile	ttc Phe	agc Ser	ata Ile	aca Thr	agt Ser 170	ttt Phe	tta Leu	aag Lys	aat Asn	gga Gly 175	gta Val	gcc Ala	caa Gln	584					
caa Gln 180	att Ile	gat Asp	gaa Glu	aaa Lys	caa Gln	gcc Ala 185	atc Ile	att Ile	cct Pro	aat Asn	aac Asn 190	ttg Leu	ttg Leu	cat His	ttt Phe	632					
gat Asp 195	aag Lys	cac His	tac Tyr	aaa Lys	cgc Arg	att Ile 200	ttt Phe	aaa Lys	gcc Ala	cat His 205	gat Asp	tgg Trp	ctt Leu	tat Tyr	gat Asp 210	680					
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Lys	Ile	Leu	Lys	Leu	Pro	Leu	Leu	Val	Lys	Lys	Gln	Glu	Asn	Asn	Thr	
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Met	Arg	Asp	Phe	Lys	Glu	Arg	Tyr	Lys	Ile	Glu	Lys	Leu	Tyr	Tyr	Leu	
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tta	gat	gat	aat	att	aaa	aat	ttt	gaa	ttt	gct	aag	atc	aag	cat	aaa	1256
Leu	Asp	Asp	Asn	Ile	Lys	Asn	Phe	Glu	Phe	Ala	Lys	Ile	Lys	His	Lys	
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Ile	Ser	Leu	Tyr	Phe	Lys	Asp	Ala	Lys	Phe	Tyr	Pro	Lys	Ser	Val	Ala	
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Lys	Thr	Phe	Asn	Asp	Cys	Gly	Leu	Val	Leu	Glu	Arg	Gln	Lys	Ser	Asp	
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Leu	Tyr	Lys	Glu	Cys	Leu	Pro	Lys	Leu	Ser	Met	Glu	Val	Val	Lys	Asp	
	500					505					510					



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ttt gta aaa tta gag cta aaa aat caa agc ttc aac aat atc cca cct Phe Val Lys Leu Glu Leu Lys Asn Gln Ser Phe Asn Asn Ile Pro Pro	3032





Glu Phe Ala Thr Pro Phe Lys Glu Tyr Leu Lys Arg Leu Glu Glu Tyr  
805 810 815  
Tyr Phe Asp Pro Gln Thr Asp Arg Asp Phe Lys Lys Gly Leu Leu Asp  
820 825 830  
Phe Phe Ser Arg Leu Asn Asp Ser Ile Pro Ala Lys Leu Gln Gln Glu  
835 840 845  
Phe Ile Asn Leu Pro Ser Thr Asp Phe Leu Ser Arg Cys Leu Gly Ser  
850 855 860  
Leu Glu Lys Asp Phe Gln Lys Thr Ile Phe Lys Lys Leu Lys Val Thr  
865 870 875 880  
Asn Leu Lys Thr Leu Ser Ile Val Ala Arg Ala Ser Trp Asn Asn Glu  
885 890 895  
Lys Phe Leu Glu Asn Leu Met Ala Gln Thr Ser Leu Glu Gln Gln Lys  
900 905 910  
Asp Phe Leu Lys Arg Ile Glu Glu Cys Leu Lys Asn Pro Glu Ser Phe  
915 920 925  
Tyr Phe Ser Ser Ala Cys Glu Leu Leu Leu Ala Phe Leu Ser Tyr Arg  
930 935 940  
Asn Ala Lys Arg Glu Leu Glu Leu Ile Pro Glu Ser Glu Lys Thr Met  
945 950 955 960  
Arg Leu Leu Asp Ser Ile Asp Lys Ala Ile Glu Lys Glu Thr Glu Ile  
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agt ttt gtc atc aaa atg aag ttt ttt aaa gaa aaa gaa aaa gaa gtt 96  
Ser Phe Val Ile Lys Met Lys Phe Phe Lys Glu Lys Glu Lys Glu Val  
20 25 30  
tca aaa att aaa agt ttg aga aag ttt gag tca aat ccg cta gta aga 144  
Ser Lys Ile Lys Ser Leu Arg Lys Phe Glu Ser Asn Pro Leu Val Arg  
35 40 45  
ttt gac cct agc gct ctt gcg cta gag cca aaa ttt tagtataatg 190  
Phe Asp Pro Ser Ala Leu Ala Leu Glu Pro Lys Phe  
50 55 60  
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 35 40 45  
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 aca atg aac gct cct aaa gac ata gaa aac cca aaa aaa tgg ctc aac 104  
 Thr Met Asn Ala Pro Lys Asp Ile Glu Asn Pro Lys Lys Trp Leu Asn  
 5 10 15  
 cct gct gcg ctg caa aca atc act aaa atc gtg cct ata aaa att tca 152  
 Pro Ala Ala Leu Gln Thr Ile Thr Lys Ile Val Pro Ile Lys Ile Ser  
 20 25 30  
 ggc agg cgc gtg tct ttt gct tgc tct aag atg aga tta gcc cct ttt 200  
 Gly Arg Arg Val Ser Phe Ala Cys Ser Lys Met Arg Leu Ala Pro Phe  
 35 40 45 50  
 ttt cca ggc aat aat aaa aga act aaa ata atc cct gct gaa ata aag 248  
 Phe Pro Gly Asn Asn Lys Arg Thr Lys Ile Ile Pro Ala Glu Ile Lys  
 55 60 65  
 gtt tta aga atg agt aaa tta aca tta gaa tct tta cta cct aga ata 296  
 Val Leu Arg Met Ser Lys Leu Thr Leu Glu Ser Leu Leu Pro Arg Ile  
 70 75 80  
 gtg agg att aaa agc atg gga atg gct gca ata tct tgg aaa atc aaa 344  
 Val Arg Ile Lys Ser Met Gly Met Ala Ala Ile Ser Trp Lys Ile Lys  
 85 90 95  
 atc ccc acc gcg ctc ttt ccc atg ggc gtg cta agc tgt ttg gaa tct 392  
 Ile Pro Thr Ala Leu Phe Pro Met Gly Val Leu Ser Cys Leu Glu Ser  
 100 105 110  
 tca aag aat ttc agc aca ata gcg gtt gaa gag agc gaa agc ccc atg 440  
 Ser Lys Asn Phe Ser Thr Ile Ala Val Glu Glu Ser Glu Ser Pro Met  
 115 120 125 130

cct aaa aca agg gaa aaa atg ggt gaa aga ccc aaa aca aaa tac ccc Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys Tyr Pro 135 140 145	488
aat aaa aaa gcg att aaa gcg cat aaa acc act tgt aaa agc cca aaa Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser Pro Lys 150 155 160	536
acc agc act tct tgt ttg atg gat ttg agc ttg tca aaa tta aac tca Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu Asn Ser 165 170 175	584
atg cct atc ata aac att aaa aag acg ata cca aat tcg cca ata tca Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro Ile Ser 180 185 190	632
gac aac aaa tca aaa tca tta att tta aaa aaa gcc gct aag acc gtt Asp Asn Lys Ser Lys Ser Leu Ile Leu Lys Lys Ala Ala Lys Thr Val 195 200 205 210	680
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Pro Phe Phe Pro Gly Asn Asn Lys Arg Thr Lys Ile Ile Pro Ala Glu 50 55 60	
Ile Lys Val Leu Arg Met Ser Lys Leu Thr Leu Glu Ser Leu Leu Pro 65 70 75 80	
Arg Ile Val Arg Ile Lys Ser Met Gly Met Ala Ala Ile Ser Trp Lys 85 90 95	
Ile Lys Ile Pro Thr Ala Leu Phe Pro Met Gly Val Leu Ser Cys Leu 100 105 110	
Glu Ser Ser Lys Asn Phe Ser Thr Ile Ala Val Glu Glu Ser Glu Ser 115 120 125	
Pro Met Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys 130 135 140	
Tyr Pro Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser 145 150 155 160	
Pro Lys Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu 165 170 175	
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Thr Val Pro Val Gln Met  
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Leu Glu Asn Leu Ser Gln Gln Lys Ile Leu Gln Leu Ser Gly Gly Gln  
5 10 15

gcc caa cga gtc gct tta gca aga gct tta atc gca gcc aag aat cta 152  
Ala Gln Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu  
20 25 30

ttg ctt tta gat gag cct tta aac gcc tta gat aac gcc tta aaa aac 200  
Leu Leu Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn  
35 40 45 50

gaa gtg caa caa ggt ttg ctt gat ttt atc aag cgt gaa aat tta agc 248  
Glu Val Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser  
55 60 65

gtg tta ttg gta agc cat aac ccc aat gaa atc acc aag ctc gcg caa 296  
Val Leu Leu Val Ser His Asn Pro Asn Glu Ile Thr Lys Leu Ala Gln  
70 75 80

act ttc ctc ttt tta aac aat ggc gtt att gat cct aat caa gaa aat 344  
Thr Phe Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn  
85 90 95

cgg ctt ttt tca aac cgc tta tta ata aaa cct ctc ttt gaa gat gaa 392  
Arg Leu Phe Ser Asn Arg Leu Leu Ile Lys Pro Leu Phe Glu Asp Glu  
100 105 110

aat tat tgc cat tat gag gtc att tct caa acg att agt ttg ccc aaa 440  
Asn Tyr Cys His Tyr Glu Val Ile Ser Gln Thr Ile Ser Leu Pro Lys  
115 120 125 130

gat tgt ctg aac cca act ttt aag ctt gat ttc aat caa aac aaa aaa 488  
Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp Phe Asn Gln Asn Lys Lys  
135 140 145

ttt tagaaatatt ttttcatttt cctcttaaaa ccctcttatt tttcaaaagg 541  
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<210> 346  
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<212> PRT

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<212> DNA

<213> Helicobacter pylori

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<221> CDS

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Leu	Ile	Val	Thr	Arg	Phe	Ala	Pro	Ser	Pro	Thr	Gly	Tyr	Leu	His	Ile		
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gga	ggc	tta	aga	aca	gcc	att	ttc	aat	tat	ctt	ttt	gca	cga	gcc	aat		153
Gly	Gly	Leu	Arg	Thr	Ala	Ile	Phe	Asn	Tyr	Leu	Phe	Ala	Arg	Ala	Asn		
	20					25					30						
caa	gga	aaa	ttt	ttt	tta	cgc	att	gaa	gac	acg	gat	ttg	agc	cgt	aac		201
Gln	Gly	Lys	Phe	Phe	Leu	Arg	Ile	Glu	Asp	Thr	Asp	Leu	Ser	Arg	Asn		
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Ser	Ile	Glu	Ala	Ala	Asn	Ala	Ile	Ile	Glu	Ala	Phe	Lys	Trp	Val	Gly		
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Leu	Glu	Tyr	Asp	Gly	Glu	Ile	Leu	Tyr	Gln	Ser	Lys	Arg	Phe	Glu	Ile		
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tat	aaa	gaa	tac	att	caa	aaa	ctc	tta	gat	gaa	gac	aaa	gcc	tat	tat		345

Tyr	Lys	Glu	Tyr	Ile	Gln	Lys	Leu	Leu	Asp	Glu	Asp	Lys	Ala	Tyr	Tyr		
		85					90					95					
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Cys	Tyr	Met	Ser	Lys	Glu	Glu	Leu	Asp	Ala	Leu	Arg	Glu	Glu	Gln	Lys		
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gcc	agg	aaa	gaa	acc	cca	cgc	tat	gac	aat	cgc	tat	cgt	gat	ttt	aaa		441
Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp	Phe	Lys		
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Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys	Val	Pro		
				135					140					145			
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Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu	Val	Lys		
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Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser	Asp	Gly		
		165					170					175					
aca	ccc	act	tat	aac	ttt	gtg	gtt	act	att	gat	gac	gct	tta	atg	ggg		633
Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu	Met	Gly		
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Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr	Pro	Lys		
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caa	atc	gtt	ctt	tat	aag	gct	ttg	aat	ttt	aaa	atc	cct	aat	ttt	ttc		729
Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn	Phe	Phe		
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His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser	Lys	Arg		
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His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr	Leu	Lys		
		245					250					255					
gaa	gct	tta	gtg	aat	ttt	tta	gcg	cgt	ttg	ggg	tgg	agc	tat	cag	gat		873
Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr	Gln	Asp		
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Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp	Pro	Lys		
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Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu	Asn	Trp		
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Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu	Leu	Lys		
			310					315					320				

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325 330 335	
caa ttg gat cgc ttg tta gac gct ctc aaa gaa aga tct caa aca cta	1113
Gln Leu Asp Arg Leu Leu Asp Ala Leu Lys Glu Arg Ser Gln Thr Leu	
340 345 350	
aaa gaa tta gcc ctt aaa ata gat gag gtt tta atc gcc cct gtg gag	1161
Lys Glu Leu Ala Leu Lys Ile Asp Glu Val Leu Ile Ala Pro Val Glu	
355 360 365 370	
tat gaa gaa aag gtt ttt aaa aaa ctc aat caa gcg ctc gtt atg ccc	1209
Tyr Glu Glu Lys Val Phe Lys Lys Leu Asn Gln Ala Leu Val Met Pro	
375 380 385	
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390 395 400	
gaa agc gcg cta gaa aac gcc atg cgc caa atc att gaa gaa gaa aag	1305
Glu Ser Ala Leu Glu Asn Ala Met Arg Gln Ile Ile Glu Glu Glu Lys	
405 410 415	
att aaa gcg ggt agt ttt atg cag cct tta aga ttg gcc ctt ttg ggt	1353
Ile Lys Ala Gly Ser Phe Met Gln Pro Leu Arg Leu Ala Leu Leu Gly	
420 425 430	
aag gga ggc ggg ata ggc ctt aaa gaa gcg ctt ttt att tta ggc aaa	1401
Lys Gly Gly Gly Ile Gly Leu Lys Glu Ala Leu Phe Ile Leu Gly Lys	
435 440 445 450	
aca gag agc gtc aaa aga ata gag gat ttt ttg aaa aac taaaaaattg	1450
Thr Glu Ser Val Lys Arg Ile Glu Asp Phe Leu Lys Asn	
455 460	
gctctgtttt cattgggtat taaaataaaa gagtttgatt ttagcgggttg ttaagcaact	1510
ccttttgaaa aataagagg	1530
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<211> 463	
<212> PRT	
<213> Helicobacter pylori	
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1 5 10 15	
His Ile Gly Gly Leu Arg Thr Ala Ile Phe Asn Tyr Leu Phe Ala Arg	
20 25 30	
Ala Asn Gln Gly Lys Phe Phe Leu Arg Ile Glu Asp Thr Asp Leu Ser	
35 40 45	
Arg Asn Ser Ile Glu Ala Ala Asn Ala Ile Ile Glu Ala Phe Lys Trp	
50 55 60	
Val Gly Leu Glu Tyr Asp Gly Glu Ile Leu Tyr Gln Ser Lys Arg Phe	
65 70 75 80	
Glu Ile Tyr Lys Glu Tyr Ile Gln Lys Leu Leu Asp Glu Asp Lys Ala	
85 90 95	
Tyr Tyr Cys Tyr Met Ser Lys Glu Glu Leu Asp Ala Leu Arg Glu Glu	
100 105 110	

Gln Lys Ala Arg Lys Glu Thr Pro Arg Tyr Asp Asn Arg Tyr Arg Asp  
115 120 125  
Phe Lys Gly Thr Pro Pro Lys Gly Ile Glu Pro Val Val Arg Ile Lys  
130 135 140  
Val Pro Gln Asn Glu Val Ile Gly Phe Asn Asp Gly Val Lys Gly Glu  
145 150 155 160  
Val Lys Val Asn Thr Asn Glu Leu Asp Asp Phe Ile Ile Ala Arg Ser  
165 170 175  
Asp Gly Thr Pro Thr Tyr Asn Phe Val Val Thr Ile Asp Asp Ala Leu  
180 185 190  
Met Gly Ile Thr Asp Val Ile Arg Gly Asp Asp His Leu Ser Asn Thr  
195 200 205  
Pro Lys Gln Ile Val Leu Tyr Lys Ala Leu Asn Phe Lys Ile Pro Asn  
210 215 220  
Phe Phe His Val Pro Met Ile Leu Asn Glu Glu Gly Gln Lys Leu Ser  
225 230 235 240  
Lys Arg His Gly Ala Thr Asn Val Met Asp Tyr Gln Glu Met Gly Tyr  
245 250 255  
Leu Lys Glu Ala Leu Val Asn Phe Leu Ala Arg Leu Gly Trp Ser Tyr  
260 265 270  
Gln Asp Lys Glu Val Phe Ser Met Gln Glu Leu Leu Glu Leu Phe Asp  
275 280 285  
Pro Lys Asp Leu Asn Ser Ser Pro Ser Cys Phe Ser Trp His Lys Leu  
290 295 300  
Asn Trp Leu Asn Ala His Tyr Leu Lys Asn Gln Ser Val Gln Glu Leu  
305 310 315 320  
Leu Lys Leu Leu Lys Pro Phe Ser Phe Ser Asp Leu Ser His Leu Asn  
325 330 335  
Pro Thr Gln Leu Asp Arg Leu Leu Asp Ala Leu Lys Glu Arg Ser Gln  
340 345 350  
Thr Leu Lys Glu Leu Ala Leu Lys Ile Asp Glu Val Leu Ile Ala Pro  
355 360 365  
Val Glu Tyr Glu Glu Lys Val Phe Lys Lys Leu Asn Gln Ala Leu Val  
370 375 380  
Met Pro Leu Leu Glu Lys Phe Lys Leu Glu Leu Asn Lys Ala Asn Phe  
385 390 395 400  
Asn Asp Glu Ser Ala Leu Glu Asn Ala Met Arg Gln Ile Ile Glu Glu  
405 410 415  
Glu Lys Ile Lys Ala Gly Ser Phe Met Gln Pro Leu Arg Leu Ala Leu  
420 425 430  
Leu Gly Lys Gly Gly Gly Ile Gly Leu Lys Glu Ala Leu Phe Ile Leu  
435 440 445  
Gly Lys Thr Glu Ser Val Lys Arg Ile Glu Asp Phe Leu Lys Asn  
450 455 460

<210> 349  
<211> 382  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (51)...(329)

<400> 349  
cctaagtatt ttttctatct tgccccctt atgtgttaga aaattctaaa atg ttt  
Met Phe  
1

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aag ggg att tat cct atg cgt aat ttt cct atc cac cat aat ggt ttt      104
Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn Gly Phe
      5                      10                      15

aaa cat gaa gtg tta gct cac atg cta aaa agg cat aaa gag cca ttt      152
Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu Pro Phe
      20                      25                      30

att tta agc tat aat gac tgc gaa ttt gta agg aat gct tat aaa gat      200
Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr Lys Asp
      35                      40                      45                      50

ttt aaa att tta gaa cca tct tgg caa tac act atg gga caa ggc gag      248
Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln Gly Glu
      55                      60                      65

atc aga atg ggt aaa aat cgc tta gaa aga ggc gat aat aac cat gtc      296
Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn His Val
      70                      75                      80

aaa caa tct cat gag tta ttg att atc aag gag taaaaatgca tattagcgaa      349
Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu
      85                      90

gtcaaaactg cctttaaaat cgctgatgta gaa      382

<210> 350
<211> 93
<212> PRT
<213> Helicobacter pylori

<400> 350
Met Phe Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn
 1                      5                      10                      15
Gly Phe Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu
      20                      25                      30
Pro Phe Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr
      35                      40                      45
Lys Asp Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln
      50                      55                      60
Gly Glu Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn
      65                      70                      75                      80
His Val Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu
      85                      90

<210> 351
<211> 376
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (183)...(323)

<400> 351
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actattttga gttcttacta tcattaacca cttttaattg ttatgaattg agtttgattg      120
ataggggtga ttatagcatt tatggggcaa aaaaagtaga atctgtatca agttttatta      180
ag atg cat gcg gta aaa tcc gct aaa tca agg agt gtt att atg gaa      227

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Met His Ala Val Lys Ser Ala Lys Ser Arg Ser Val Ile Met Glu
 1          5          10          15
gca gac gca acc aca cta tta gga ttt ttt gaa gaa aat caa aac aat      275
Ala Asp Ala Thr Thr Leu Leu Gly Phe Phe Glu Glu Asn Gln Asn Asn
          20          25          30
caa ttt gtc att cct atc tat cag agg ttg tat agt tgg aaa aag gaa      323
Gln Phe Val Ile Pro Ile Tyr Gln Arg Leu Tyr Ser Trp Lys Lys Glu
          35          40          45
taatgcgaac aattatggga tgatattata aaaattggtg ggaatgataa gat      376

<210> 352
<211> 47
<212> PRT
<213> Helicobacter pylori

<400> 352
Met His Ala Val Lys Ser Ala Lys Ser Arg Ser Val Ile Met Glu Ala
 1          5          10          15
Asp Ala Thr Thr Leu Leu Gly Phe Phe Glu Glu Asn Gln Asn Asn Gln
          20          25          30
Phe Val Ile Pro Ile Tyr Gln Arg Leu Tyr Ser Trp Lys Lys Glu
          35          40          45

<210> 353
<211> 1021
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(968)

<400> 353
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                               Met Arg
                               1
ctt tat caa aaa caa ggc ttg gaa atg gtg ggt caa aag ttg gat tct      104
Leu Tyr Gln Lys Gln Gly Leu Glu Met Val Gly Gln Lys Leu Asp Ser
          5          10          15
tat tta gcg gat aaa tct ttt tgg gca gaa gaa ctt caa aac aag gac      152
Tyr Leu Ala Asp Lys Ser Phe Trp Ala Glu Glu Leu Gln Asn Lys Asp
          20          25          30
acg gat ttt ggc tat tat caa aac aag cag ttt tta ttt gtg gct aat      200
Thr Asp Phe Gly Tyr Tyr Gln Asn Lys Gln Phe Leu Phe Val Ala Asn
          35          40          45          50
aaa tcc aag ccc agt ttg gag ttt tat gag ata gaa aat aac atg ctt      248
Lys Ser Lys Pro Ser Leu Glu Phe Tyr Glu Ile Glu Asn Asn Met Leu
          55          60          65
aaa aaa atc aac agc tct aaa gct ctt gta ggc tct aaa aag ggc gat      296
Lys Lys Ile Asn Ser Ser Lys Ala Leu Val Gly Ser Lys Lys Gly Asp
          70          75          80

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aag act tta gag ggc gat ttg gcc acg cct att gga gtg tat cgt atc Lys Thr Leu Glu Gly Asp Leu Ala Thr Pro Ile Gly Val Tyr Arg Ile 85 90 95	344
acg cag aaa tta gag cgc ttg gat caa tat tat ggc gtt ttg gct ttt Thr Gln Lys Leu Glu Arg Leu Asp Gln Tyr Tyr Gly Val Leu Ala Phe 100 105 110	392
gta acg aat tac cct aat ttg tat gat acc ttg aaa aaa cgc acc ggg Val Thr Asn Tyr Pro Asn Leu Tyr Asp Thr Leu Lys Lys Arg Thr Gly 115 120 125 130	440
cat ggc att tgg gtg cat gga atg cct tta aat ggc gat cgg aat gaa His Gly Ile Trp Val His Gly Met Pro Leu Asn Gly Asp Arg Asn Glu 135 140 145	488
ttg aac acc aag ggc tgt att gcg att gaa aac ccg ctt tta agc tct Leu Asn Thr Lys Gly Cys Ile Ala Ile Glu Asn Pro Leu Leu Ser Ser 150 155 160	536
tat gac aaa gtg tta aaa ggc gaa aaa gcg ttc ctc atc acc tat gaa Tyr Asp Lys Val Leu Lys Gly Glu Lys Ala Phe Leu Ile Thr Tyr Glu 165 170 175	584
gac aag ttt ttc cca agc acc aaa gaa gaa ttg agc atg att tta agc Asp Lys Phe Phe Pro Ser Thr Lys Glu Glu Leu Ser Met Ile Leu Ser 180 185 190	632
tcc ctt ttt caa tgg aaa gaa gcc tgg gct agg ggc gat ttt gaa cgc Ser Leu Phe Gln Trp Lys Glu Ala Trp Ala Arg Gly Asp Phe Glu Arg 195 200 205 210	680
tac atg cgt ttt tat aac ccc aat ttc act cgc tat gac ggc atg aaa Tyr Met Arg Phe Tyr Asn Pro Asn Phe Thr Arg Tyr Asp Gly Met Lys 215 220 225	728
ttt aac gct ttt aaa gag tat aaa aaa agg gtg ttt gca aaa aac gaa Phe Asn Ala Phe Lys Glu Tyr Lys Lys Arg Val Phe Ala Lys Asn Glu 230 235 240	776
aaa aag aat atc gct ttt tcc tct atc aat gtg atc cct tac ccc aac Lys Lys Asn Ile Ala Phe Ser Ser Ile Asn Val Ile Pro Tyr Pro Asn 245 250 255	824
tct cag aac aaa cgc ttg ttt tat gtg gtg ttt gac caa gat tat aaa Ser Gln Asn Lys Arg Leu Phe Tyr Val Val Phe Asp Gln Asp Tyr Lys 260 265 270	872
gcc tac cag cat aac aag ctc tct tat agc tcc aat tct caa aaa gaa Ala Tyr Gln His Asn Lys Leu Ser Tyr Ser Ser Asn Ser Gln Lys Glu 275 280 285 290	920
ctc tat ata gag att gaa aac aat caa gtg tct att ata atg gaa aaa Leu Tyr Ile Glu Ile Glu Asn Asn Gln Val Ser Ile Ile Met Glu Lys 295 300 305	968
taagaaaaat agggcctttgt tttaattagg ataatctaag cggatttttc taa	1021



<210> 354  
 <211> 306  
 <212> PRT  
 <213> Helicobacter pylori

<400> 354

Met	Arg	Leu	Tyr	Gln	Lys	Gln	Gly	Leu	Glu	Met	Val	Gly	Gln	Lys	Leu
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Asp	Ser	Tyr	Leu	Ala	Asp	Lys	Ser	Phe	Trp	Ala	Glu	Glu	Leu	Gln	Asn
			20					25					30		
Lys	Asp	Thr	Asp	Phe	Gly	Tyr	Tyr	Gln	Asn	Lys	Gln	Phe	Leu	Phe	Val
		35					40					45			
Ala	Asn	Lys	Ser	Lys	Pro	Ser	Leu	Glu	Phe	Tyr	Glu	Ile	Glu	Asn	Asn
	50					55					60				
Met	Leu	Lys	Lys	Ile	Asn	Ser	Ser	Lys	Ala	Leu	Val	Gly	Ser	Lys	Lys
65					70					75					80
Gly	Asp	Lys	Thr	Leu	Glu	Gly	Asp	Leu	Ala	Thr	Pro	Ile	Gly	Val	Tyr
				85					90					95	
Arg	Ile	Thr	Gln	Lys	Leu	Glu	Arg	Leu	Asp	Gln	Tyr	Tyr	Gly	Val	Leu
			100					105						110	
Ala	Phe	Val	Thr	Asn	Tyr	Pro	Asn	Leu	Tyr	Asp	Thr	Leu	Lys	Lys	Arg
		115					120					125			
Thr	Gly	His	Gly	Ile	Trp	Val	His	Gly	Met	Pro	Leu	Asn	Gly	Asp	Arg
	130					135						140			
Asn	Glu	Leu	Asn	Thr	Lys	Gly	Cys	Ile	Ala	Ile	Glu	Asn	Pro	Leu	Leu
145					150					155					160
Ser	Ser	Tyr	Asp	Lys	Val	Leu	Lys	Gly	Glu	Lys	Ala	Phe	Leu	Ile	Thr
			165						170					175	
Tyr	Glu	Asp	Lys	Phe	Phe	Pro	Ser	Thr	Lys	Glu	Glu	Leu	Ser	Met	Ile
		180						185					190		
Leu	Ser	Ser	Leu	Phe	Gln	Trp	Lys	Glu	Ala	Trp	Ala	Arg	Gly	Asp	Phe
		195					200					205			
Glu	Arg	Tyr	Met	Arg	Phe	Tyr	Asn	Pro	Asn	Phe	Thr	Arg	Tyr	Asp	Gly
	210					215					220				
Met	Lys	Phe	Asn	Ala	Phe	Lys	Glu	Tyr	Lys	Lys	Arg	Val	Phe	Ala	Lys
225					230					235					240
Asn	Glu	Lys	Lys	Asn	Ile	Ala	Phe	Ser	Ser	Ile	Asn	Val	Ile	Pro	Tyr
			245						250					255	
Pro	Asn	Ser	Gln	Asn	Lys	Arg	Leu	Phe	Tyr	Val	Val	Phe	Asp	Gln	Asp
			260					265					270		
Tyr	Lys	Ala	Tyr	Gln	His	Asn	Lys	Leu	Ser	Tyr	Ser	Ser	Asn	Ser	Gln
		275					280					285			
Lys	Glu	Leu	Tyr	Ile	Glu	Ile	Glu	Asn	Asn	Gln	Val	Ser	Ile	Ile	Met
	290					295					300				
Glu	Lys														
305															

<210> 355  
 <211> 990  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (43)...(870)

<400> 355

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 Met Phe Lys Asp

54

ttt tat cgc acc acc ctc tct ttt tta aag cct tta ttg ctt tta cta	102
Phe Tyr Arg Thr Thr Leu Ser Phe Leu Lys Pro Leu Leu Leu Leu Leu	
5 10 15 20	
ggt tta tta ttg ccg ttt tca ctt tgt ata gct gat gaa tat att agc	150
Val Leu Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp Glu Tyr Ile Ser	
25 30 35	
ata agt gat gat tgg gat gaa att gtg cga aat cat aag aca tat tat	198
Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His Lys Thr Tyr Tyr	
40 45 50	
ttt gaa aat ggt tta gac cat ttt aat caa ggc caa tac cag caa gcc	246
Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln Tyr Gln Gln Ala	
55 60 65	
ttt aaa gat ttt aga ttg gcg caa gaa tac agc atc ggg ctt ggc agt	294
Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile Gly Leu Gly Ser	
70 75 80	
ggt tat tta gcc aaa atg tat ttg gag gga aag ggc gtg aaa gtg gat	342
Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly Val Lys Val Asp	
85 90 95 100	
tac aaa aaa gca caa ttt tat gca gaa aac gct atc aaa ggg tat ggg	390
Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile Lys Gly Tyr Gly	
105 110 115	
agc gga ttg tta ggg ggt gct ctt att tta gga cgc atg caa gca gaa	438
Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg Met Gln Ala Glu	
120 125 130	
ggc tta ggg atg aaa aag gat ttg aaa caa gcg ctc aag act tat agg	486
Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu Lys Thr Tyr Arg	
135 140 145	
cat gtg gtt cgc atg ttt tct aat aaa agc aca aat ttt gct aac aat	534
His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn Phe Ala Asn Asn	
150 155 160	
ttt aga tta cca aac ctt gcg gaa ttt act agt atg ctt att gga tcg	582
Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met Leu Ile Gly Ser	
165 170 175 180	
cga ttc att gat ctt tca ggt ttg agc gcg aat cct ata aaa ttt gga	630
Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro Ile Lys Phe Gly	
185 190 195	
aag aaa ttt gga ata ctt gtt aag aaa tcc act caa atc aaa gat aag	678
Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln Ile Lys Asp Lys	
200 205 210	
aca ctt ctt tgg gaa gat att gct gaa att tca agc aat att act tta	726
Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser Asn Ile Thr Leu	
215 220 225	
ctc aaa caa caa atg ggg gag atc ctt tat agg att ggg atc gct tat	774



[illegible]

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Leu	Asp	Cys	Val	Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys	
1				5					10					15		
gag	aaa	tta	ctc	acc	cct	gaa	gcg	aga	aaa	ctc	tta	gaa	gaa	gct	aaa	96
Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys	
			20					25					30			
gag	agc	gtt	aaa	gct	tat	aaa	gac	tgc	gta	tca	aaa	gct	agg	aat	gaa	144
Glu	Ser	Val	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu	
		35					40					45				
aaa	gag	aaa	aaa	gaa	tgc	gag	aaa	tta	ctc	acg	cct	gaa	gcg	aaa	aaa	192
Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	
	50					55					60					
ctt	tta	gag	caa	caa	gtg	cta	gat	tgt	ttg	aaa	aac	gct	aaa	acc	gaa	240
Leu	Leu	Glu	Gln	Gln	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Glu	
65					70					75					80	
gct	gat	aaa	aaa	agg	tgt	gtc	aaa	gat	ctc	cct	aaa	gac	ttg	cag	aaa	288
Ala	Asp	Lys	Lys	Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys	
				85					90					95		
aag	gtt	tta	gct	aaa	gag	agc	gtt	aag	gct	tat	ttg	gac	tgc	gta	tca	336
Lys	Val	Leu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	
			100					105					110			
aga	gct	agg	aat	gaa	aaa	gag	aaa	aaa	gaa	tgc	gag	aaa	ttg	ctc	acc	384
Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	
			115				120					125				
cct	gaa	gcg	aaa	aaa	ctt	tta	gaa	gaa	gcc	aaa	gag	agt	ctt	aaa	gct	432
Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	
	130					135					140					
tat	aaa	gac	tgc	ctc	tct	caa	gct	aga	aat	gaa	gaa	gaa	agg	aga	gct	480
Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	
145					150					155					160	
tgc	gag	aaa	cta	ctc	acg	cct	gaa	gcg	aga	aaa	ctc	tta	gag	caa	gaa	528
Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	
			165						170					175		
gtt	aag	aaa	agc	att	aag	gct	tat	ttg	gac	tgc	gta	tca	aga	gct	agg	576
Val	Lys	Lys	Ser	Ile	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	
			180					185					190			
aat	gaa	aaa	gag	aaa	aaa	gaa	tgc	gag	aaa	tta	ctc	acg	cct	gaa	gcg	624
Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Le					

aga Arg	aaa Lys 210	ttt Phe	tta Leu	gcg Ala	aag Lys	caa Gln 215	gtg Val	cta Leu	aat Asn	tgt Cys	ttg Leu 220	gaa Glu	aaa Lys	gct Ala	gga Gly	672
aat Asn 225	gaa Glu	gaa Glu	gaa Glu	aga Arg	aaa Lys 230	gca Ala	tgt Cys	ctt Leu	aaa Lys	aat Asn 235	ctc Leu	cct Pro	aaa Lys	gac Asp	tta Leu 240	720
cag Gln	gaa Glu	aat Asn	att Ile	tta Leu 245	gct Ala	aaa Lys	gag Glu	agt Ser	ctt Leu 250	aaa Lys	gct Ala	tat Tyr	aaa Lys	gac Asp 255	tgc Cys	768
ctc Leu	tct Ser	caa Gln	gct Ala 260	aga Arg	aat Asn	gaa Glu	gaa Glu	gaa Glu 265	agg Arg	aga Arg	gct Ala	tgc Cys	gag Glu 270	aaa Lys	cta Leu	816
ctc Leu	acg Thr	cct Pro 275	gaa Glu	gcg Ala	aga Arg	aaa Lys	ctc Leu 280	tta Leu	gag Glu	caa Gln	gaa Glu	gtt Val 285	aag Lys	aaa Lys	agc Ser	864
gtt Val	aag Lys 290	gct Ala	tat Tyr	ttg Leu	gac Asp	tgc Cys 295	gta Val	tca Ser	aga Arg	gct Ala	agg Arg 300	aat Asn	gaa Glu	aaa Lys	gag Glu	912
aaa Lys 305	aaa Lys	gaa Glu	tgc Cys	gag Glu	aaa Lys 310	tta Leu	ctc Leu	acg Thr	cct Pro	gaa Glu 315	gcg Ala	aga Arg	aaa Lys	ttt Phe	tta Leu 320	960
gcg Ala	aaa Lys	gaa Glu	ctc Leu	caa Gln 325	caa Gln	aaa Lys	gat Asp	aaa Lys	gcg Ala 330	atc Ile	aaa Lys	gat Asp	tgc Cys	ttg Leu 335	aaa Lys	1008
aac Asn	gcc Ala	gat Asp	cct Pro 340	aac Asn	gac Asp	aga Arg	gcg Ala	gct Ala 345	atc Ile	atg Met	aag Lys	tgt Cys	ttg Leu 350	gat Asp	ggt Gly	1056
ttg Leu	agc Ser	gat Asp 355	gaa Glu	gag Glu	aag Lys	ctc Leu	aaa Lys 360	tac Tyr	ctg Leu	caa Gln	gaa Glu	gct Ala 365	aga Arg	gaa Glu	aag Lys	1104
gct Ala	gtt Val 370	gcg Ala	gat Asp	tgt Cys	ttg Leu	gct Ala 375	atg Met	gct Ala	aaa Lys	acc Thr	gat Asp 380	gaa Glu	gaa Glu	aaa Lys	agg Arg	1152
aaa Lys 385	tgc Cys	caa Gln	aac Asn	ctt Leu	tat Tyr 390	agc Ser	gat Asp	ttg Leu	atc Ile	caa Gln 395	gaa Glu	atc Ile	caa Gln	aat Asn	aaa Lys 400	1200
agg Arg	aca Thr	caa Gln	aac Asn	aaa Lys 405	caa Gln	aat Asn	caa Gln	ttg Leu	agt Ser 410	aaa Lys	aca Thr	gaa Glu	agg Arg	ttg Leu 415	cat His	1248
caa Gln	gca Ala	agc Ser	gag Glu 420	tgc Cys	ttg Leu	gat Asp	aac Asn	tta Leu 425	gat Asp	gac Asp	cct Pro	act Thr	gat Asp 430	caa Gln	gag Glu	1296
gcc Ala	ata Ile	gag Glu	caa Gln	tgt Cys	tta Leu	gag Glu	ggc Gly	ttg Leu	agc Ser	gat Asp	agt Ser	gaa Glu	agg Arg	gcg Ala	cta Leu	1344

435			440			445										
att Ile	cta Leu	gga Gly	att Ile	aaa Lys	cga Arg	caa Gln	gct Ala	gat Asp	gaa Glu	gtg Val	gat Asp	ctg Leu	att Ile	tat Tyr	agc Ser	1392
450			455			460										
gat Asp	cta Leu	aga Arg	aac Asn	cgt Arg	aaa Lys	acc Thr	ttt Phe	gat Asp	aac Asn	atg Met	gcg Ala	gct Ala	aaa Lys	ggt Gly	tat Tyr	1440
465			470			475										
cca Pro	ttg Leu	tta Leu	cca Pro	atg Met	gat Asp	ttc Phe	aaa Lys	aat Asn	ggc Gly	ggc Gly	gat Asp	att Ile	gcc Ala	act Thr	att Ile	1488
485			490			495										
aac Asn	gcc Ala	act Thr	aat Asn	gtt Val	gat Asp	gcg Ala	gac Asp	aaa Lys	ata Ile	gct Ala	agc Ser	gat Asp	aat Asn	cct Pro	att Ile	1536
500			505			510										
tat Tyr	gct Ala	tcc Ser	ata Ile	gag Glu	cct Pro	gat Asp	att Ile	gcc Ala	aag Lys	caa Gln	tac Tyr	gaa Glu	aca Thr	gaa Glu	aaa Lys	1584
515			520			525										
acc Thr	att Ile	aag Lys	gat Asp	aag Lys	aat Asn	tta Leu	gaa Glu	gct Ala	aaa Lys	tta Leu	gct Ala	aag Lys	gct Ala	tta Leu	ggt Gly	1632
530			535			540										
ggc Gly	aat Asn	aaa Lys	aaa Lys	gat Asp	gac Asp	gat Asp	aaa Lys	gaa Glu	aaa Lys	agt Ser	aaa Lys	aaa Lys	tcc Ser	aca Thr	gca Ala	1680
545			550			555										
gaa Glu	gct Ala	aaa Lys	gca Ala	gaa Glu	aac Asn	aat Asn	aag Lys	ata Ile	gac Asp	aaa Lys	gat Asp	gtc Val	gca Ala	gaa Glu	act Thr	1728
565			570			575										
gcc Ala	aag Lys	aat Asn	atc Ile	agt Ser	gaa Glu	atc Ile	gct Ala	ctt Leu	aag Lys	aac Asn	aaa Lys	aaa Lys	gaa Glu	aag Lys	agt Ser	1776
580			585			590										
ggg Gly	gaa Glu	ttt Phe	gta Val	gat Asp	gaa Glu	aat Asn	ggt Gly	aat Asn	ccc Pro	att Ile	gat Asp	gac Asp	aaa Lys	aag Lys	aaa Lys	1824
595			600			605										
gca Ala	gaa Glu	aaa Lys	caa Gln	gat Asp	gaa Glu	aca Thr	agc Ser	cct Pro	gtc Val	aaa Lys	cag Gln	gcc Ala	ttt Phe	ata Ile	ggc Gly	1872
610			615			620										
aag Lys	agt Ser	gat Asp	ccc Pro	aca Thr	ttt Phe	gtt Val	tta Leu	gcg Ala	caa Gln	tac Tyr	acc Thr	ccc Pro	att Ile	gaa Glu	atc Ile	1920
625			630			635										
act Thr	ctg Leu	act Thr	tct Ser	aaa Lys	gta Val	gat Asp	gcc Ala	act Thr	ctc Leu	aca Thr	ggt Gly	ata Ile	gtg Val	agt Ser	ggg Gly	1968
645			650			655										
gtt Val	gta Val	gcc Ala	aaa Lys	gat Asp	gta Val	tgg Trp	aac Asn	atg Met	aac Asn	ggc Gly	act Thr	atg Met	atc Ile	tta Leu	tta Leu	2016
660			665			670										
gac	aaa	ggc	act	aag	gtg	tat	ggg	aat	tat	caa	agc	gtg	aaa	ggt	ggc	2064

Asp	Lys	Gly	Thr	Lys	Val	Tyr	Gly	Asn	Tyr	Gln	Ser	Val	Lys	Gly	Gly					
		675					680					685								
aca	ccc	att	atg	aca	cgc	tta	atg	ata	gtc	ttt	act	aaa	gcc	att	acg	2112				
Thr	Pro	Ile	Met	Thr	Arg	Leu	Met	Ile	Val	Phe	Thr	Lys	Ala	Ile	Thr					
	690					695					700									
cct	gat	ggg	gtg	ata	ata	cct	cta	gca	aac	gct	caa	gca	gca	ggc	atg	2160				
Pro	Asp	Gly	Val	Ile	Ile	Pro	Leu	Ala	Asn	Ala	Gln	Ala	Ala	Gly	Met					
705					710					715					720					
ttg	ggg	gaa	gca	ggg	gta	gat	ggc	tat	gtg	aat	aat	cac	ttt	atg	aag	2208				
Leu	Gly	Glu	Ala	Gly	Val	Asp	Gly	Tyr	Val	Asn	Asn	His	Phe	Met	Lys					
				725					730					735						
cgc	ata	ggc	ttt	gct	gtg	ata	gca	agc	gtg	gtt	aat	agc	ttc	ttg	caa	2256				
Arg	Ile	Gly	Phe	Ala	Val	Ile	Ala	Ser	Val	Val	Asn	Ser	Phe	Leu	Gln					
			740					745					750							
act	gcg	cct	atc	ata	gct	cta	gat	aaa	ctc	ata	ggc	ctt	ggc	aaa	ggg	2304				
Thr	Ala	Pro	Ile	Ile	Ala	Leu	Asp	Lys	Leu	Ile	Gly	Leu	Gly	Lys	Gly					
		755				760						765								
aga	agt	gaa	agg	aca	cct	gaa	ttt	aat	tac	gct	ttg	ggg	caa	gct	atc	2352				
Arg	Ser	Glu	Arg	Thr	Pro	Glu	Phe	Asn	Tyr	Ala	Leu	Gly	Gln	Ala	Ile					
	770					775					780									
aat	ggg	agc	atg	caa	agt	tca	gct	cag	atg	tct	aat	caa	att	cta	ggg	2400				
Asn	Gly	Ser	Met	Gln	Ser	Ser	Ala	Gln	Met	Ser	Asn	Gln	Ile	Leu	Gly					
785					790					795					800					
caa	ctg	atg	aat	atc	ccc	cca	agt	ttt	tac	aaa	aac	gag	ggc	gat	agt	2448				
Gln	Leu	Met	Asn	Ile	Pro	Pro	Ser	Phe	Tyr	Lys	Asn	Glu	Gly	Asp	Ser					
				805					810					815						
att	aag	att	ctc	aca	atg	gac	gat	att	gat	ttt	agc	ggg	gtg	tat	gat	2496				
Ile	Lys	Ile	Leu	Thr	Met	Asp	Asp	Ile	Asp	Phe	Ser	Gly	Val	Tyr	Asp					
			820					825					830							
gtt	aaa	att	act	aac	aaa	tct	gtg	gta	gat	gaa	att	atc	aaa	caa	agc	2544				
Val	Lys	Ile	Thr	Asn	Lys	Ser	Val	Val	Asp	Glu	Ile	Ile	Lys	Gln	Ser					
		835					840					845								
acc	aaa	act	ttg	tct	aga	gaa	cat	gaa	gaa	atc	acc	aca	agc	ccc	aaa	2592				
Thr	Lys	Thr	Leu	Ser	Arg	Glu	His	Glu	Glu	Ile	Thr	Thr	Ser	Pro	Lys					
	850					855					860									
ggg	ggc	aat	taattcaaga gaaaggataa aatatattca tggtactaaa													2641				
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865																				
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<210> 358  
 <211> 867  
 <212> PRT  
 <213> Helicobacter pylori  
  
 <400> 358

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Glu	Lys	Leu	Leu 20	Thr	Pro	Glu	Ala	Arg 25	Lys	Leu	Leu	Glu	Glu 30	Ala	Lys
Glu	Ser	Val	Lys	Ala	Tyr	Lys	Asp 40	Cys	Val	Ser	Lys	Ala 45	Arg	Asn	Glu
Lys	Glu 50	Lys	Lys	Glu	Cys	Glu 55	Lys	Leu	Leu	Thr	Pro 60	Glu	Ala	Lys	Lys
Leu 65	Leu	Glu	Gln	Gln	Val 70	Leu	Asp	Cys	Leu	Lys 75	Asn	Ala	Lys	Thr	Glu 80
Ala	Asp	Lys	Lys	Arg 85	Cys	Val	Lys	Asp 90	Leu	Pro	Lys	Asp	Leu 95	Gln	Lys
Lys	Val	Leu	Ala 100	Lys	Glu	Ser	Val	Lys 105	Ala	Tyr	Leu	Asp	Cys 110	Val	Ser
Arg	Ala	Arg 115	Asn	Glu	Lys	Glu	Lys 120	Lys	Glu	Cys	Glu	Lys 125	Leu	Leu	Thr
Pro	Glu 130	Ala	Lys	Lys	Leu	Leu 135	Glu	Glu	Ala	Lys	Glu 140	Ser	Leu	Lys	Ala
Tyr 145	Lys	Asp	Cys	Leu	Ser 150	Gln	Ala	Arg	Asn	Glu 155	Glu	Glu	Arg	Arg	Ala 160
Cys	Glu	Lys	Leu	Leu 165	Thr	Pro	Glu	Ala	Arg 170	Lys	Leu	Leu	Glu 175	Gln	Glu
Val	Lys	Lys	Ser 180	Ile	Lys	Ala	Tyr	Leu 185	Asp	Cys	Val	Ser	Arg 190	Ala	Arg
Asn	Glu	Lys 195	Glu	Lys	Lys	Glu	Cys 200	Glu	Lys	Leu	Leu	Thr 205	Pro	Glu	Ala
Arg	Lys 210	Phe	Leu	Ala	Lys	Gln 215	Val	Leu	Asn	Cys	Leu 220	Glu	Lys	Ala	Gly
Asn 225	Glu	Glu	Glu	Arg	Lys 230	Ala	Cys	Leu	Lys	Asn 235	Leu	Pro	Lys	Asp	Leu 240
Gln	Glu	Asn	Ile	Leu 245	Ala	Lys	Glu	Ser	Leu 250	Lys	Ala	Tyr	Lys	Asp 255	Cys
Leu	Ser	Gln	Ala 260	Arg	Asn	Glu	Glu	Glu 265	Arg	Arg	Ala	Cys	Glu 270	Lys	Leu
Leu	Thr	Pro 275	Glu	Ala	Arg	Lys	Leu 280	Leu	Glu	Gln	Glu	Val 285	Lys	Lys	Ser
Val	Lys 290	Ala	Tyr	Leu	Asp	Cys 295	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu
Lys 305	Lys	Glu	Cys	Glu	Lys 310	Leu	Leu	Thr	Pro	Glu 315	Ala	Arg	Lys	Phe	Leu 320
Ala	Lys	Glu	Leu	Gln 325	Gln	Lys	Asp	Lys	Ala 330	Ile	Lys	Asp	Cys	Leu 335	Lys
Asn	Ala	Asp	Pro 340	Asn	Asp	Arg	Ala	Ala 345	Ile	Met	Lys	Cys	Leu 350	Asp	Gly
Leu	Ser	Asp 355	Glu	Glu	Lys	Leu	Lys	Tyr	Leu	Gln	Glu	Ala 365	Arg	Glu	Lys
Ala	Val	Ala	Asp	Cys	Leu	Ala 375	Met	Ala	Lys	Thr	Asp	Glu	Glu	Lys	Arg
Lys 385	Cys	Gln	Asn	Leu	Tyr 390	Ser	Asp	Leu	Ile	Gln 395	Glu	Ile	Gln	Asn	Lys
Arg	Thr	Gln	Asn	Lys 405	Gln	Asn	Gln	Leu	Ser	Lys	Thr	Glu	Arg	Leu 415	His
Gln	Ala	Ser	Glu	Cys	Leu	Asp	Asn	Leu 425	Asp	Asp	Pro	Thr	Asp	Gln	Glu
Ala	Ile	Glu	Gln	Cys	Leu	Glu	Gly 440	Leu	Ser	Asp	Ser	Glu	Arg	Ala	Leu
Ile	Leu	Gly	Ile	Lys	Arg	Gln 455	Ala	Asp	Glu	Val	Asp	Leu	Ile	Tyr	Ser
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<222> (65)...(688)

<400> 359

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ttga atg gcc gtt tat tta gat ttt gaa aat cat att aaa gag att caa	109
Met Ala Val Tyr Leu Asp Phe Glu Asn His Ile Lys Glu Ile Gln	
1 5 10 15	
aat gaa att gaa tta gcc ctt att aga ggc gat gag gac gct aaa gaa	157
Asn Glu Ile Glu Leu Ala Leu Ile Arg Gly Asp Glu Asp Ala Lys Glu	
20 25 30	
atc tta gaa aaa aga ttg gat aag gag gtt aaa agc att tat tcc aat	205
Ile Leu Glu Lys Arg Leu Asp Lys Glu Val Lys Ser Ile Tyr Ser Asn	
35 40 45	
ctc act gat ttt caa aaa ctc caa tta gca aga cac cct gac aga ccc	253
Leu Thr Asp Phe Gln Lys Leu Gln Leu Ala Arg His Pro Asp Arg Pro	
50 55 60	
tac gct atg gat tac att gat ctc atc tta aaa gat aaa tat gaa gtc	301
Tyr Ala Met Asp Tyr Ile Asp Leu Ile Leu Lys Asp Lys Tyr Glu Val	
65 70 75	
ttt ggg gat agg cat tat aac gat gat aaa gcg atc gtg tgc ttt gta	349
Phe Gly Asp Arg His Tyr Asn Asp Asp Lys Ala Ile Val Cys Phe Val	
80 85 90 95	
ggg aaa att gat aat gtc cca gtt gtg gtg atc gga gaa gaa aag ggc	397
Gly Lys Ile Asp Asn Val Pro Val Val Val Ile Gly Glu Glu Lys Gly	
100 105 110	
aga ggg act aaa aac aaa ctc tta aga aat ttt ggc atg cct aac cct	445
Arg Gly Thr Lys Asn Lys Leu Leu Arg Asn Phe Gly Met Pro Asn Pro	
115 120 125	
tgt ggc tat cgt aag gct ttg aaa atg gca aag ttt gct gaa aag ttt	493
Cys Gly Tyr Arg Lys Ala Leu Lys Met Ala Lys Phe Ala Glu Lys Phe	
130 135 140	
aat ttg cct att tta atg ctt gtg gat aca gcc ggg gcg tat ccg ggg	541
Asn Leu Pro Ile Leu Met Leu Val Asp Thr Ala Gly Ala Tyr Pro Gly	
145 150 155	
att ggt gca gaa gaa agg ggg caa agt gaa gcg atc gct aaa aat ctc	589
Ile Gly Ala Glu Glu Arg Gly Gln Ser Glu Ala Ile Ala Lys Asn Leu	
160 165 170 175	
caa gag ttc gcc tct tta aaa gtc cct act att tct gta att atc ggt	637
Gln Glu Phe Ala Ser Leu Lys Val Pro Thr Ile Ser Val Ile Ile Gly	
180 185 190	
gag ggg ggc agt ggt ggt gcg cta cga ttg cag tgg ctg aca aat tgg	685
Glu Gly Gly Ser Gly Gly Ala Leu Arg Leu Gln Trp Leu Thr Asn Trp	
195 200 205	
cta tgatggaata ttccattttt agcggttatat cccagaagg ttgtgcggcg	738
attctttggg atgaccctag caagactgaa gtggctatta aagcgatgaa aatcacgcct	798
agagacttaa aggaggcggg gcttattgat gatattatct tagagcctag caaaggggct	858

catagagaca aatttttcag

877

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<212> PRT  
<213> Helicobacter pylori

<400> 360

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20 25 30  
Leu Glu Lys Arg Leu Asp Lys Glu Val Lys Ser Ile Tyr Ser Asn Leu  
35 40 45  
Thr Asp Phe Gln Lys Leu Gln Leu Ala Arg His Pro Asp Arg Pro Tyr  
50 55 60  
Ala Met Asp Tyr Ile Asp Leu Ile Leu Lys Asp Lys Tyr Glu Val Phe  
65 70 75 80  
Gly Asp Arg His Tyr Asn Asp Asp Lys Ala Ile Val Cys Phe Val Gly  
85 90 95  
Lys Ile Asp Asn Val Pro Val Val Val Ile Gly Glu Glu Lys Gly Arg  
100 105 110  
Gly Thr Lys Asn Lys Leu Leu Arg Asn Phe Gly Met Pro Asn Pro Cys  
115 120 125  
Gly Tyr Arg Lys Ala Leu Lys Met Ala Lys Phe Ala Glu Lys Phe Asn  
130 135 140  
Leu Pro Ile Leu Met Leu Val Asp Thr Ala Gly Ala Tyr Pro Gly Ile  
145 150 155 160  
Gly Ala Glu Glu Arg Gly Gln Ser Glu Ala Ile Ala Lys Asn Leu Gln  
165 170 175  
Glu Phe Ala Ser Leu Lys Val Pro Thr Ile Ser Val Ile Ile Gly Glu  
180 185 190  
Gly Gly Ser Gly Gly Ala Leu Arg Leu Gln Trp Leu Thr Asn Trp Leu  
195 200 205

<210> 361  
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<212> DNA  
<213> Helicobacter pylori

<220>

<221> CDS

<222> (67)...(744)

<400> 361

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Met Gln Phe Thr Gly Lys Asn Val Leu Ile Thr Gly Ala Ser  
1 5 10  
aaa ggc att ggg gct gaa atc gcc aaa act ctc gct tct atg ggg ctg 156  
Lys Gly Ile Gly Ala Glu Ile Ala Lys Thr Leu Ala Ser Met Gly Leu  
15 20 25 30  
aaa gtt tgg atc aat tac cgc agt aat gct gaa gtg gct gac gct ttg 204  
Lys Val Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu  
35 40 45  
aaa aat gag ctt gaa gaa aaa ggc tat aag gca gct gtc att aaa ttt 252

Lys	Asn	Glu	Leu	Glu	Glu	Lys	Gly	Tyr	Lys	Ala	Ala	Val	Ile	Lys	Phe	
			50					55					60			
gat	gcg	gct	tct	gaa	agc	gat	ttt	att	gaa	gcg	ata	caa	acc	atc	gtc	300
Asp	Ala	Ala	Ser	Glu	Ser	Asp	Phe	Ile	Glu	Ala	Ile	Gln	Thr	Ile	Val	
			65				70					75				
caa	agc	gat	ggg	ggg	ttg	tct	tac	ttg	gtg	aat	aac	gcc	ggg	gtg	gtg	348
Gln	Ser	Asp	Gly	Gly	Leu	Ser	Tyr	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	
	80					85				90						
cgc	gat	aaa	tta	gcg	atc	aaa	atg	aaa	aca	gaa	gac	ttt	cac	cat	gtc	396
Arg	Asp	Lys	Leu	Ala	Ile	Lys	Met	Lys	Thr	Glu	Asp	Phe	His	His	Val	
	95				100				105						110	
ata	gac	aat	aac	ctc	act	tca	gcc	ttt	ata	ggg	tgc	cga	gag	gct	tta	444
Ile	Asp	Asn	Asn	Leu	Thr	Ser	Ala	Phe	Ile	Gly	Cys	Arg	Glu	Ala	Leu	
				115					120					125		
aag	gtg	atg	agc	aag	agt	cgt	ttt	ggg	agc	gtg	gtc	aat	gtc	gct	tct	492
Lys	Val	Met	Ser	Lys	Ser	Arg	Phe	Gly	Ser	Val	Val	Asn	Val	Ala	Ser	
			130					135					140			
atc	att	ggg	gaa	aga	ggc	aat	atg	ggg	cag	aca	aac	tac	tca	gcg	agt	540
Ile	Ile	Gly	Glu	Arg	Gly	Asn	Met	Gly	Gln	Thr	Asn	Tyr	Ser	Ala	Ser	
		145				150						155				
aag	ggg	gga	atg	att	gca	atg	agc	aag	tcc	ttt	gct	tat	gag	gga	gct	588
Lys	Gly	Gly	Met	Ile	Ala	Met	Ser	Lys	Ser	Phe	Ala	Tyr	Glu	Gly	Ala	
	160					165					170					
tta	agg	aat	att	cgt	ttc	aac	tct	gta	acg	ccc	ggg	ttt	ata	gaa	acc	636
Leu	Arg	Asn	Ile	Arg	Phe	Asn	Ser	Val	Thr	Pro	Gly	Phe	Ile	Glu	Thr	
	175				180					185					190	
gac	atg	aac	gcc	aat	ttg	aaa	gac	gaa	ctc	aaa	gcg	gat	tat	gtt	aaa	684
Asp	Met	Asn	Ala	Asn	Leu	Lys	Asp	Glu	Leu	Lys	Ala	Asp	Tyr	Val	Lys	
				195				200						205		
aac	att	cct	tta	aac	agg	cta	ggg	tct	gct	aag	gaa	gtg	gca	gaa	gcg	732
Asn	Ile	Pro	Leu	Asn	Arg	Leu	Gly	Ser	Ala	Lys	Glu	Val	Ala	Glu	Ala	
			210				215						220			
gta	ggn	ttc	ttt	tgagt	gat	ca	ctctag	ttac	atcact	ggag	agact	ctc	caa			784
Val	Xaa	Phe	Phe													
			225													
agtcaatggc	gggctttata															804
<210>	362															
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1				5					10					15		
Ile	Gly	Ala	Glu	Ile	Ala	Lys	Thr	Leu	Ala	Ser	Met	Gly	Leu	Lys	Val	
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Arg Leu  
70

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373

<210> 364  
<211> 70  
<212> PRT  
<213> Helicobacter pylori

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20 25 30  
Arg Ala Arg Arg Phe Phe Glu Ser Lys Thr Glu Lys Arg Lys Lys Gln  
35 40 45  
Lys Ile Ser Ala Lys Lys Lys Val Leu Lys Arg Leu Tyr Met Leu Arg  
50 55 60  
Arg Tyr Glu Ser Arg Leu  
65 70

<210> 365  
<211> 23  
<212> DNA  
<213> Helicobacter pylori

<400> 365  
ccgaattcgg ttataaagcc cct 23

<210> 366  
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<212> DNA  
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<400> 366  
ccgctcgagt taaggctgat ttaa 24

<210> 367  
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<212> DNA  
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<400> 367  
cgcgatccg aggaaatagc atgttaataa cc 32

<210> 368  
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<400> 368  
ccgctcgagt cactgcttgc atgacttatt cca 33

106390"ET65B50